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ATTENTION: BOX PATENT APPLICATION

Sir:

Transmitted herewith for filing is the patent application of

Inventor(s): Frank P. Luyten, Malcolm Moos, and Steven Chao-Huan Chang

For: CARTILAGE-DERIVED MORPHOGENETIC PROTEINS

Enclosed are:

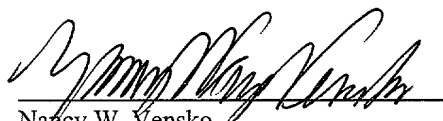
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- (X) (4) Four sheets of drawing.
- (X) Please amend the specification to read as the first sentence: --This application is a continuation of prior application 08/836,081 filed July 28, 1997 which claims priority under 35 U.S.C. § 371 to PCT/US94/12814 filed November 7, 1994.--
- (X) A paper copy of the Sequence Listing.
- (X) The Computer Readable Form (CRF) copy of the Sequence Listing of this application is identical with the CRF copy of prior application 08/836,081 filed July 28, 1997. As permitted by 37 CFR 1.821(e) and (f), please use the CRF copy that is already on file for the other application in lieu of filing a CRF copy for this application. As required by 37 CFR 1.821(e) and (f), I hereby certify that the data of the CRF copy filed for the other application and the paper copy of the Sequence Listing filed in this application are the same.
- (X) A copy of Declaration from prior application is enclosed.
- (X) Please amend the title to read --DNA MOLECULES ENCODING CARTILAGE-DERIVED MORPHOGENETIC PROTEINS--
- (X) Please use the attached abstract which is on a separate sheet of paper to meet the requirement that the application contain an abstract of the disclosure.
- (X) Please amend the specification as follows:
Page 3, line 24, after "nucleotide" insert--(SEQ ID NO: 11)--.
Page 3, line 24, after "amino acid sequence" insert --(SEQ ID NO: 13)--.
Page 3, line 26, after "nucleotide" insert --(SEQ ID NO: 12)--.
Page 3, line 26, after "amino acid sequence" insert --(SEQ ID NO: 14)--.
- (X) Incorporation by Reference. The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.
- (X) Return prepaid postcard.

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Basic Fee			\$690	\$690
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Independent Claims	6 - 3 =	3 ×	\$78	\$234
If application contains any multiple dependent claims(s), then add			\$260	\$
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CARTILAGE-DERIVED MORPHOGENETIC PROTEINS

Field of the Invention

The present invention relates generally to the field of cartilage and bone development. More specifically, the invention relates to cartilage-derived morphogenetic proteins that stimulate development and repair of cartilage *in vivo*.

Background of the Invention

Bone morphogenetic proteins (BMPs) are members of the TGF- β superfamily that can induce endochondral bone formation in adult animals. This superfamily includes a large group of structurally related signaling proteins that are secreted as dimers and then cleaved to result in biologically active carboxy terminal domains of the proteins. These bioactive proteins are characterized by 7 highly conserved cysteine residues. Interestingly, these proteins have different roles at various stages of embryogenesis and in adult animals. Recombinant BMPs are now available and have been shown to induce endochondral bone formation when assayed *in vivo*.

Indeed, the initial discovery of the BMPs was facilitated by such *in vivo* assays for cartilage and bone development. These assays were based on the observation that bone development could be initiated by subcutaneous or intramuscular implantation of compositions comprising an extract of demineralized bone and residual bone powder. The novel proteins identified in the extracts were termed "bone morphogenetic proteins." These proteins were subsequently classified as members of the TGF- β superfamily by virtue of amino acid sequence relatedness. Screening of genomic and cDNA libraries led to the isolation of polynucleotides encoding BMP-2, -3, -4, -5, -6 and -7.

One deficiency of the bone induction assay regards its inability to distinguish the physiological roles of different BMP family members. The cartilage and bone inducing activity of the BMPs is remarkable because the normal stages of endochondral bone formation that occur during ontogeny are recapitulated in the adult animal. These stages include mesenchymal condensation, cartilage and bone and bone marrow formation and eventual mineralization to produce mature bone.

Several observations suggest that BMPs have wide-ranging extraskeletal roles in development. First, localization studies in both human and mouse tissues have demonstrated high levels of mRNA expression and protein synthesis for various BMPs in kidney (BMPs -3, -4, -7), lung (BMPs -3, -4, -5, -6), small intestine (BMPs -3, -4, -7), heart (BMPs -2, -4, -6, -7), limb bud (BMPs -2, -4, -5, -7) and teeth (BMPs -3, -4, -7). Second, several members of the family, including BMP-4 and -7, are key molecules in epithelial-mesenchymal interactions, for instance during odontogenesis. Third, BMP-2 and BMP-4 are involved in the signaling pathway that controls patterning in the developing chick limb and BMP-4 is a ventralizing factor in early *Xenopus* development. Fourth, *Drosophila* homologs of the BMPs, the decapentaplegic (dpp) and

60 A gene products, have the capacity to induce bone in mammals whereas human BMP-4 confers normal embryonic dorso-ventral patterning in *Drosophila* transformants defective in dpp expression. Thus, the BMPs are now appreciated as pleiotropic cytokines.

Interestingly, none of the known BMPs are strongly expressed in the chondroblasts and
5 chondrocytes of the cartilage core of developing long bones. The hypertrophic chondrocytes, where both Vgr-1 (BMP-6, (Lyons et al., *Development* 109:833 (1990)) and OP-1 (BMP-7)(Vukicevic et al., *Biochem. Biophys. Res. Commun.* 198:693 (1994)) have been found are exceptions in this regard.

Summary of the Invention

10 One aspect of the present invention is a purified cartilage extract that stimulates local cartilage formation when combined with a matrix and implanted into a mammal. This extract can conveniently be produced by a method which includes the steps of: obtaining cartilage tissue; homogenizing the cartilage tissue in the presence of chaotropic agents under conditions that permit separation of proteins from proteoglycans; separating the proteins from the proteoglycans and then
15 obtaining the proteins. The step for separating the proteins from the proteoglycans can be carried out using a sepharose column. The extract can also be obtained by additionally including the steps of separating the proteins on a molecular sieve and then collecting the proteins having molecular weights in the 30 kDa to 60 kDa size range. Articular cartilage or epiphyseal cartilage can be used in the preparation of this purified extract.

20 A second aspect of the present invention is a method of preparing a partially purified articular cartilage extract having chondrogenic activity. This method includes the steps of first obtaining cartilage tissue; homogenizing the cartilage tissue in the presence of chaotropic agents under conditions that permit separation of proteins from proteoglycans; separating the proteins from the proteoglycans and finally obtaining the proteins. The separation of proteins and
25 proteoglycans can be accomplished using a sepharose column. In particular, the step for separating proteins from proteoglycans can include isolating the proteins that bind heparin Sepharose in the presence of 0.15 M NaCl but not in the presence of 1 M NaCl. An additional step in the purification procedure can include separating the proteins on a molecular sieve and then obtaining the proteins having molecular weights between 30 kDa and 60 kDa.

30 A third aspect of the present invention is an isolated DNA molecule that encodes a protein having chondrogenic activity *in vivo* but substantially no osteogenic activity *in vivo*. More particularly, this aspect of the invention regards a molecule having a nucleotide sequence that can hybridize to a polynucleotide which has the nucleotide sequence SEQ ID NO:11 or SEQ ID NO:12 at 55°C with 0.4× SSC and 0.1% SDS. The proteins encoded by such DNA molecules can have
35 the amino acid sequences of SEQ ID NO:13 or SEQ ID NO:14.

A forth aspect of the present invention is a recombinant protein having chondrogenic activity *in vivo* but substantially no osteogenic activity *in vivo*. This protein can have the amino acid sequence of SEQ ID NO:13 or SEQ ID NO:14.

5 A fifth aspect of the present invention is a method of stimulating cartilage formation in a mammal. This method includes the steps: supplying cartilage-derived morphogenetic proteins having *in vivo* chondrogenic activity; mixing the partially purified proteins with a matrix to produce a product that facilitates administration of the partially purified proteins and implanting this mixture into the body of mammal to stimulate cartilage formation at the site of implantation. The partially purified cartilage-derived morphogenetic proteins can be obtained from either
10 articular cartilage or epiphyseal cartilage. The matrix can also include non-cellular material. Viable chondroblast or chondrocytes can also be included in the mixture prior to implantation. The mixture can be implanted either subcutaneously or intramuscularly.

A sixth aspect of the present invention is a composition that can be administered to a mammal for the purpose of stimulating chondrogenic activity at the site of administration without
15 substantially stimulating osteogenic activity. This composition comprises at least one cartilage-derived morphogenetic protein and a matrix. The cartilage-derived morphogenetic protein can be derived from an extract of either articular cartilage or epiphyseal cartilage. In another embodiment, the cartilage-derived morphogenetic protein is a recombinant protein. This recombinant protein can have the amino acid sequence of either SEQ ID NO:13 or SEQ ID NO:14.
20 The matrix used to create the composition can be either fibrin glue, freeze-dried cartilage, collagens or the guanidinium-insoluble collagenous residue of demineralized bone. Alternatively the matrix can be a non-resorbable matrix such as tetracalcium phosphate or hydroxyapatite.

Brief Description of the Figures

Figure 1 presents the nucleotide and predicted amino acid sequence encoded by the full
25 length human CDMP-1 cDNA.

Figure 2 presents the nucleotide and predicted amino acid sequence encoded by the bovine CDMP-2.

Figure 3 presents the genetic maps of chromosome 2 showing the localization of CDMP-1. The map on the right is based on the data from two separate crosses.

30 Figure 4 shows an alignment of segments from predicted CDMP amino acid sequences in standard one letter code.

Detailed Description of the Invention

We discovered that partially purified extracts of newborn calf articular cartilage contained an activity that induced cartilage formation when implanted subcutaneously in rats. This biological
35 activity was reminiscent of that which characterized the BMPs. Degenerate oligonucleotide primer sets derived from the highly conserved carboxy-terminal region of the BMP family were employed

in reverse transcription-polymerase chain reactions (RT-PCR) using poly(A)⁺ RNA from articular cartilage as a template. These procedures allowed us to determine which BMPs were expressed in chondrocytes.

Two novel members of the TGF- β superfamily were identified and designated Cartilage-Derived Morphogenetic Protein-1 (CDMP-1), and -2 (CDMP-2). The C-terminal TGF- β domains of these proteins were 82% identical, thus defining a novel subfamily most closely related to BMP-5, BMP-6 and osteogenic protein-1. Northern analyses showed that postnatally both genes were predominantly expressed in cartilaginous tissues. *In situ* hybridization and immunostaining of sections from human embryos showed that CDMP-1 was predominantly found at the stage of precartilaginous mesenchymal condensation and throughout the cartilaginous cores of the developing long bones. CDMP-2 expression was restricted to the hypertrophic chondrocytes of ossifying long bone centers. Neither gene was detectable in the axial skeleton during human embryonic development. The cartilage-specific localization pattern of these novel TGF- β superfamily members, which contrasts with the more ubiquitous presence of other BMP family members, suggested a role for these proteins in chondrocyte differentiation and growth of long bones.

The discovery of a novel subfamily of cartilage derived morphogenetic proteins suggested the existence of morphogens that primarily functioned in the induction and maintenance (i.e., balancing cartilage and bone formation at articular surfaces) of cartilaginous and bony tissues. This subfamily may also include key molecules that govern bone marrow differentiation.

The cartilage-derived morphogenetic proteins contained in the cartilage extract of the present invention, and the recombinant CDMP-1 and CDMP-2 proteins described herein are contemplated for use in the therapeutic induction and maintenance of cartilage. For example, local injection of CDMPs as soluble agents is contemplated for the treatment of subglottic stenosis, tracheomalacia, chondromalacia patellae and osteoarthritic disease. Other contemplated utilities include healing of joint surface lesions (e.g. temporomandibular joint lesions or lesions induced posttraumatically or by osteochondritis) using biological delivery systems such as fibrin glue, freeze-dried cartilage grafts, and collagens mixed with CDMPs and locally applied to fill the lesion. Such mixtures can also be enriched with viable cartilage progenitor cells, chondroblasts or chondrocytes. We also contemplate repair or reconstruction of cartilaginous tissues using resorbable or non-resorbable matrices (tetracalcium phosphate, hydroxyapatite) or biodegradable polymers (PLG, polylactic acid/polyglycolic acid) coated or mixed with CDMPs. Such compositions may be used in maxillofacial and orthopedic reconstructive surgery. Finally, the CDMPs disclosed herein have utility as growth factors for cells of the chondrocyte lineage *in vitro*. Cells expanded *ex vivo* can be implanted into an individual at a site where chondrogenesis is desired.

We also anticipate the polynucleotides disclosed herein will also have utility as diagnostic reagents for detecting genetic abnormalities associated genes encoding CDMs. Diagnostic testing could be performed prenatally using material obtained during amniocentesis. Any of several genetic screening procedures could be adapted for use with probes enabled by the present invention. These procedures include restriction fragment length polymorphism (RFLP), ligase chain reaction (LCR) or polymerase chain reaction (PCR).

We began our investigations by considering whether there were differences between the chondrogenic/osteogenic differentiation factors that characterized calcifying (epiphyseal, scapular cartilage) and non-calcifying (articular, nasal septum) cartilage tissues. It had been previously established that tail tendon, achilles tendon, cartilage and skin matrices were devoid of chondrogenic/osteogenic activity (originally described as "transforming potency") as measured in an *in vivo* subcutaneous implantation model in rats (Reddi A.H., 1976, "Collagen and Cell differentiation" in *Biochemistry of Collagen*, eds. Ramachandran G.N. and Reddi, A.H., pp449-478, Plenum Press, New York and London.).

We confirmed the absence of chondrogenic or osteogenic activity in crude 4 M guanidine HCl (GdnHCl) extracts of cartilage matrices, but unexpectedly discovered *in vivo* chondrogenic activity in the 0.15 M NaCl eluate of the cartilage extracts after ion exchange chromatography. The development of a unique extraction procedure (1.2 M GdnHCl and 0.5% CHAPs) followed by a heparin Sepharose affinity chromatography step confirmed the presence of *in vivo* chondrogenic activity in cartilaginous tissues. This was especially true in bovine articular and epiphyseal cartilage. When the bioactive heparin Sepharose eluates (1M NaCl eluate) were further purified using previously established procedures, molecular sieve chromatography and Con A affinity chromatography steps followed by SDS polyacrylamide gel electrophoresis and gel elution, chondrogenic activity was established. Implantation of 0.5 to 1 µg gel eluted material resulted in *in vivo* chondrogenesis. Surprisingly, and in contrast to the bone matrix purified activity, none of the peptide sequences that were found in tryptic digests of the highly purified cartilage extracts corresponded to any of the known BMPs. However, the biological activity present in the extracts was reminiscent of BMP-like activity by virtue of its loss of activity upon reduction and alkylation, its affinity for heparin Sepharose and Con A.

Although other materials and methods similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are now described. General references for methods that can be used to perform the various nucleic acid manipulations and procedures described herein can be found in *Molecular Cloning: A Laboratory Manual* (Sambrook et al. eds. Cold Spring Harbor Lab Publ. 1989) and *Current Protocols in Molecular Biology* (Ausubel et al. eds., Greene Publishing Associates and Wiley-Interscience 1987). The disclosures contained in these references are hereby incorporated by

reference. A description of the experiments and results that led to the creation of the present invention follows.

We initially discovered that an extract of cartilage possessed a unique chondrogenic activity. In particular, we discovered that newborn articular cartilage contained chondrogenic activities when assayed in the *in vivo* subcutaneous implantation model. Using a procedure adapted from that used for the isolation of BMPs from demineralized bone matrix, we partially purified this activity and thereby provided evidence for the presence of BMP-like molecules in cartilage.

Example 1 describes the biochemical methods used to characterize a chondrogenic activity present in bovine cartilage.

Example 1

Characterization of Cartilage Derived

Chondrogenic Activity

Articular (metatarsophalangeal joints), scapular and nasal cartilage (300 grams wet weight per tissue) were prepared from newborn calves. Epiphyseal cartilage was dissected from fetal bovine femurs (7-8 months). The tissues were finely minced and homogenized with a Polytron (top speed, 2 x 30 seconds) in 20 volumes of 1.2 M GdnHCl, 0.5% CHAPS, 50 mM Tris-HCl pH 7.2, containing protease inhibitors and extracted overnight at 4°C as described by Luyten et al., in *J. Biol. Chem.* 264:13377 (1989), which is hereby incorporated by reference. The disclosure of this article is hereby incorporated by reference. Sorgente et al., (*Biochem Biophys. Acta.* 282:441 (1972)) disclosed these procedures extract >90% of the lower molecular weight matrix while leaving most of the high molecular weight proteoglycans behind. The extracts were concentrated and exchanged with 6 M urea by diafiltration using an Ultrasette™ (Filtron Technology Inc., MA) and loaded on a 0.5L heparin Sepharose (Pharmacia/LKB, NJ) column. Thereafter, the column was washed with 5 bed volumes of 6 M urea, Tris HCl pH 7.4 with 0.15 M NaCl, and then eluted with 2 vol 1 M NaCl in the same buffer. Chondrogenic activity was assayed by reconstituting a portion of the eluate with 25 mg of guanidine-insoluble collagenous residue of demineralized rat bone matrix according to procedures described by Luyten et al., in *J. Biol. Chem.* 264:13377 (1989). Implants were recovered after 10 days and alkaline phosphatase activity was measured as a biochemical indicator of cartilage and/or bone formation. The specific activity was expressed as units of alkaline phosphatase/mg of protein used for reconstitution in the bioassay. Implants were also examined histologically for evidence of cartilage formation using standard procedures known to those of ordinary skill in the art.

Additional purification steps were also performed. The 1 M NaCl eluate of articular cartilage, which contained biological activity, was concentrated by diafiltration and loaded onto a Sephacryl S-200 HR gel filtration column (XK 50/100, Pharmacia/LKB, NJ). After molecular

sieve chromatography, the bioactive fractions were pooled and exchanged with 50 mM Hepes, pH 7.4, containing 0.15 M NaCl, 10 mM MgSO₄, 1mM CaCl₂ and 0.1% (w/v) CHAPS using Macrosep™ concentrators (Filtron Technology Inc., Northborough, MA). The equilibrated sample was mixed with 1 ml Con A Sepharose (Pharmacia-LKB) previously washed with 20 volumes of the same buffer according to the procedure described by Paralkar et al., in *Biochem. Biophys. Res. Comm.* 131:37 (1989). After overnight incubation on an orbital shaker at 4°C, the slurry was packed into a disposable 0.7 cm ID Bio-Rad column and washed with 20 volumes of the Hepes buffer to remove unbound proteins. Bound proteins were eluted with 20 volumes of the same buffer containing 500 mM methyl-D-mannopyranoside. The eluate was concentrated to 200 µl using Macrosep™ concentrators. Macromolecules were then precipitated overnight with 9 volumes of absolute ethanol at 4°C. The precipitate was redissolved in 1 ml 6 M urea, Tris HCl pH 7.4. The bioactive bound protein was then mixed with 2 X Laemmli sample buffer (without reducing agents) and electrophoresed on a 12% preparative SDS/polyacrylamide gel. Gel elution of the separated protein fractions and testing for biological activity was performed as described by Luyten et al., in *J. Biol. Chem.* 264:13377 (1989). We also observed that, after reduction with dithiothreitol and alkylation with iodoacetamide, substantially all of the cartilage-forming activity contained in the protein sample was lost.

Results indicated that each of the crude extracts of the different cartilaginous tissues (articular, nasal, scapular or epiphyseal) were inactive when tested directly in the *in vivo* cartilage and bone inducing assay. This finding confirmed previously described results published by Reddi in "Collagen and Cell differentiation" in *Biochemistry of Collagen* (eds. Ramachandran G.N. and Reddi, A.H., pp449-478, Plenum Press, New York and London (1976)). However, after heparin affinity chromatography (Sampath et al., *Proc. Natl. Acad. Sci. U.S.A.* 84:7109 (1987)), chondrogenic activity was recovered in the 1 M NaCl eluate from articular cartilage extracts. An additional molecular sieve chromatography step (S200) was required to recover chondrogenic activity from epiphyseal cartilage extracts. Similar results were obtained upon ion exchange chromatography using DEAE Sephadex (0.15 M NaCl eluate). Significantly, no activity was detected in the extracts of the other cartilaginous tissues.

The highest specific activity was obtained for material derived from articular cartilage (1 U alkaline phosphatase/mg protein). This material was used for characterization of the bioactivity. Further purification of the active fraction by molecular sieve chromatography on Sephacryl S-200HR (specific activity 112 U/mg), and affinity chromatography on Concanavalin A (specific activity 480 U/mg), established the presence of cartilage and bone inducing activity characteristic of the members of the BMP family. Gel elution experiments with the Con A bound bioactive fraction demonstrated that the activity resided between roughly 34 and 38 kDa (specific activity of the gel eluted fractions was 2143 U/mg). We have also demonstrated that size separation by

molecular sieve chromatography can be used to purify biological activity in the 30-60 kDa size range. In addition, loss of activity that was observed following reduction and alkylation suggested that the bioactivity was induced either by a known or a new member(s) of the BMP family.

Given the demonstration that cartilage contained a BMP-like activity, we proceeded to isolate polynucleotides encoding the responsible proteins. Specifically, degenerate primers corresponding to conserved regions of known BMPs were designed. These primers were then employed to amplify polynucleotides using reverse transcribed mRNA from articular cartilage as a template. These procedures ultimately led to the identification of two novel cDNAs, which we called CDMP-1 and CDMP-2.

Example 2 describes the methods used to amplify polynucleotides corresponding to mRNAs that were expressed in cartilage tissue and that exhibited at least weak sequence similarity to conserved regions of the BMP mRNAs.

Example 2

PCR Amplification of cDNAs Encoding Cartilage-Derived

Morphogenetic Proteins

Total RNA from bovine articular chondrocytes (metatarsophalangeal joints) was extracted using a modified acid guanidine-phenol-chloroform method described by Chomczynski et al., in *Anal. Biochem.* 162:156 (1987) and by Luyten et al., in *Exp. Cell. Res.* 210:224 (1994). Poly(A)⁺ RNA was isolated using magnetic beads (PolyAtract™, Promega, Madison, WI). Four degenerate oligonucleotide primers corresponding to highly conserved motifs in the C-terminal region of the BMPs were used; S1: 5'-GGITGG(C/A)AIGA(C/T)TGGAT(A/C/T)(A/G)TIGC(A/C/G/T)CC-3' (SEQ ID NO:1) corresponding to amino acids [GW(Q/N)DWI(I/V)AP] (SEQ ID NO:2); S2: 5'-GGITGG(A/T)(G/C)(I)GA(G/A)TGGAT(T/C/A)ATI(A/T)G(A/C/G/T)CC-3' (SEQ ID NO:3) corresponding to amino acids [GWSEWIISP] (SEQ ID NO:4); AS1: 5'-A(A/G)(A/G)GT(C/T)TG(A/C/G/T)AC(A/G)AT(A/G)GC(A/G)TG(A/G)TT-3' (SEQ ID NO:5) corresponding to amino acids [NHAIVQTL] (SEQ ID NO:6); AS2: 5'-CAI(C/G)C(A/G)CAI(G/C)(A/C/T)I(C/T)(C/G/T)IACIA(C/T)CAT-3' (SEQ ID NO:7) corresponding to amino acids [M(V/I)V(E/R)(G/S/A)C(G/A)C] (SEQ ID NO:8). Nucleotides in parenthesis denote sites of degeneracy and I denotes inosine. First strand cDNA synthesis was performed using 1 µg Poly(A)⁺ or 5 µg total RNA with oligo dT, random hexanucleotide primers, or the antisense degenerate primers, AS1 and AS2. Successful PCR amplifications were performed with the degenerate sense primers, S1 or S2 in combination with the AS1 antisense primer were performed using conditions described by Wharton et al., in *Proc. Natl. Acad. Sci. U.S.A.* 88:9214 (1991). The reaction products were electrophoresed on 1.2% agarose gels, and DNA fragments of appropriate sizes were excised and purified using the Magic PCR Prep DNA purification system (Promega, Madison, WI). Reamplification was performed with the same primers and each PCR

product was subcloned into the PCR II vector using the TA Cloning™ System (InVitrogen Corporation, San Diego, CA). Results of RT-PCR using poly(A)⁺ RNA isolated from newborn bovine articular cartilage as template and sets of degenerate oligonucleotide primers (S1/AS1 and S1/AS2) yielded amplification products of 120 bp and 280 bp.

5 Subcloned inserts were sequenced according to the dideoxy DNA sequencing method of Sanger et al., (*Proc. Natl. Acad. Sci. U.S.A.* 74:5463 (1977)). Both DNA strands were sequenced using Sequenase Version 2.0 DNA polymerase according to manufacturer's instructions (USB, Cleveland, OH) with at least two-fold redundancy. Confirmatory data in ambiguous regions were obtained by automated thermal cycle sequencing with an Applied Biosystems Model 370A
10 sequencer and by using 7-deaza-GTP (USB, Cleveland, OH). The sequencing data were obtained from restriction fragments subcloned into pBluescript (Stratagene, La Jolla, CA) using either M13 forward and reverse primers or synthetic oligonucleotide primers.

The results from a computer-assisted search of the nucleic acid sequence databases indicated the cloned inserts encoded BMP-2, -6, BMP-7 (OP-1), and several other BMP-like
15 sequences. Identification of these latter gene fragments led us to isolate larger cDNAs that included the entire protein coding region of the transcript. The availability of such clones facilitated both a more precise analysis of the encoded BMP-like protein and permitted studies aimed at localizing the expression of these genes. Thus, cloned inserts having novel BMP-like sequences were isolated, radiolabeled and used to screen both human and bovine articular cartilage
20 cDNA libraries.

Example 3 describes the methods used to isolate human and bovine cDNAs that corresponded to a segment of one of the BMP-like gene segments that were amplified from cartilage mRNA templates.

Example 3

Library Screening

25 A 120 bp PCR fragment encoding part of the C-terminal domain of novel BMP like genes (dashed line, Figure 1) was used to screen two cDNA libraries. One library, from adolescent human articular cartilage poly(A)⁺ RNA (kindly provided by Dr. Björn Olsen, Harvard, Boston, MA), was primed with oligo dT and constructed in the λ gt11 vector. The other was a bovine oligo
30 dT and random primed articular cartilage cDNA library constructed in the UNIZAP®XR vector (Stratagene, La Jolla, CA). Approximately 1×10^6 plaques from each library were screened by standard procedures. Hybridizations were performed for 20 hours at 42°C in 6 x SSC, 1 x Denhardt's solution, 0.01% tRNA, 0.05% sodium pyrophosphate and the membranes (DuPont 137 mm nylon membranes, New England Nuclear, MA) were washed to final stringency of 6 x SSC,
35 0.1% SDS at 55°C for 20 minutes.

Thus, cloned inserts having novel BMP-like sequences were isolated, radiolabeled and used to screen both human and bovine articular cartilage cDNA libraries. Six clones were isolated from the human cDNA library. The sizes of the EcoRI inserts (2.1 kb) and their restriction maps were found to be identical for all six clones. One clone was used for nucleotide sequencing. An open reading frame encoding a BMP related protein, designated CDMP-1, was identified. It appeared that the human cDNA clone lacked the coding region for the first methionine and signal peptide. The 5' end of the human CDMP-1 was subsequently obtained from a human genomic clone isolated from a library constructed in the EMBL-3 vector (Clontech, Palo Alto, CA). The 5' end of human CDMP-1 contained a consensus translation initiation sequence disclosed by Kozak (*J. Biol. Chem.* 266:19867 (1991)) immediately followed by a putative transmembrane signal sequence described by Von Heijne (*Nucl. Acids Res.* 14:4683 (1986)). The nucleotide sequence and the translation of the open reading frame of CDMP-1 are presented in Figure 1. As shown in the figure, the CDMP-1 protein was predicted to have 500 amino acids, to consist of a pro-region of 376 amino acids, a typical cleavage site (Arg-Xaa-Xaa-Arg/Ala) (SEQ ID NO:9), and a C-terminal domain of 120 amino acids containing the seven highly conserved cysteines characteristic of the TGF- β gene family. A single N-linked glycosylation site is located in the pro-region (marked by an asterisk in the figure). A putative signal peptide is underlined in bold. A termination codon (TGA) is shown in the 5' untranslated region. The bold dashed underline indicates the fragment obtained by RT-PCR that was subsequently used to screen cDNA libraries. The 13 amino acid peptide used to raise polyclonal antibodies in rabbits is underlined. A vertical arrowhead marks the boundary between the sequence obtained from genomic DNA and cDNA.

Two clones with inserts of 2.8 kb were isolated from a bovine articular cartilage cDNA library. Both clones were sequenced and the open reading frame was found to encode another novel TGF- β related protein, designated CDMP-2. The CDMP-2 cDNA and predicted protein sequences are presented in Figure 2. As shown in the figure, the open reading frame contained a putative proteolytic processing site (boxed), preceding a 120 amino acid mature C-terminal region containing seven highly conserved cysteines. The 5' end with the first methionine and signal peptide were missing. The product obtained by RT-PCR (bold dashed underline) was used to screen a bovine cDNA articular cartilage library. The ApaI sites used to release a cDNA fragment for hybridization experiments are underlined. At the 5' end, the pro-region lacked the first methionine and signal peptide. The mature C-terminal domain of 120 amino acids showed 82% identity with CDMP-1.

Alignment of the carboxy terminal domains of CDMP-1 and -2 with other members of the BMP family revealed an amino acid identity of about 50% with BMP-5, BMP-6 and OP-1 (BMP-7). These results suggested that CDMP-1 and CDMP-2 are members of a new subfamily.

The amino acid sequence similarity between the human CDMP-1 and bovine CDMP-2 proteins prompted us to further investigate conservation of the CDMPs across different species. In particular, we employed a PCR amplification protocol to isolate CDMP cDNA sequences from a variety of species. Based on alignments of the predicted proteins encoded by these cDNAs, we identified a highly conserved amino acid sequence spanning 31 residues. Only 5 amino acid positions within this sequence showed variability. All remaining positions were identical for all isolates. As disclosed in the following Example, even the 5 variable positions showed a high degree of conservation. This structural conservation likely represents a functional domain that is characteristic of the CDMP family of proteins. Those of ordinary skill in the art will appreciate that such extraordinary amino acid sequence conservation is indicative of a functional domain. We therefore believe the consensus amino acid sequence presented in the following Example is critical to the biological activity of the CDMPs.

Example 4 describes the procedures used to identify an amino acid consensus sequence that characterizes the CDMPs from several different species.

Example 4
Identification of a Highly Conserved Consensus
Sequence in CDMP Proteins

RNA isolated from chicken sternal cartilage, bovine articular cartilage and human articular cartilage was employed as the template in RT-PCR protocols using the primers S1 and AS1 and procedures described under Example 2. Genomic DNA isolated from *Xenopus* and zebrafish was also used as the template for amplification of related gene sequences in a PCR protocol that employed the same primer sets. Amplified DNA fragments were subcloned according to standard procedures. The inserts from various isolates were sequenced by standard dideoxy chain termination protocols. Aligned segments of the predicted proteins encoded by the cloned cDNAs are presented in Figure 4.

Results of the protein alignments clearly indicated that CDMP family members from several species shared a common amino acid sequence motif in the region of the proteins encoded by the amplified cDNA segments. Of the 31 amino acid positions presented in Figure 4, all but 5 were occupied by identical amino acid residues for all of the isolates. The variable amino acids were located at positions 3, 7, 11, 16 and 18. Position 3 was occupied either by I, M or V. Position 7 was occupied by either D or E, both of which have acidic side groups. Position 11 was occupied by either Y, F or H. Position 16 was occupied by L or V, and position 18 was occupied by D or E. The consensus deduced from this alignment was:

W-I-(I/M/V)-A-P-L-(D/E)-Y-E-A-(Y/F/H)-H-C-E-G-(L/V)-C-(D/E)-F-P-L-R-S-H-L-E-P-T-N-H-A
 (SEQ ID NO:15). This consensus sequence is slightly broader than the one shown in Figure 4.

as it encompasses all the variations observed in the sequenced polynucleotides. The consensus sequence in the figure indicates predominating amino acids.

We believe that biologically active CDMPs will possess this highly conserved amino acid sequence motif. Proteins having different amino acids in the variable positions in the consensus
5 will likely represent novel family members having distinct functions. We also believe that polynucleotide hybridization probes or PCR primers designed based on this conserved protein motif can be used to isolate cDNAs encoding CDMP family members or related proteins.

Southern analyses were also carried out to investigate possible sequence conservation across species and to localize the CDMP-1 gene to a particular chromosome.

10 Example 5 describes the Southern blotting protocols used to detect DNA sequences corresponding to the CDMP-1 cDNA.

Example 5

Genetic Mapping of CDMP-1

Southern hybridization was performed using the evolutionary relatedness blot (Bios
15 Laboratories, New Haven, CT) under conditions recommended by the manufacturer. The panel of EcoRI-digested genomic DNAs included human (*homo sapiens*), mouse (*Mus musculus*), chicken (*Gallus domesticus*), frog (*Xenopus laevis*), lobster (*Homarus americanus*), mussel (*Mytilus edulis*), fish (*Tautoga onitis*), fruit fly (*Drosophila melanogaster*), nematode (*Caenorhabditis elegans*), yeast (*Saccharomyces cerevisiae*) and bacteria (*E.coli*). The 2.1 kb CDMP-1 EcoRI
20 fragment originally obtained from the cDNA library was used as a probe, and the blot was washed to a final stringency of 0.4 x SSC, 0.1% SDS, at 55°C.

Results from these Southern analyses using the original 2.1 kb human CDMP-1 cDNA probe (starting from amino acid position 40), showed 5.9 and 2.6 kb bands in humans and strong hybridization in both mouse and chicken. Fainter bands were seen in fish, frog and lobster after
25 5 days autoradiographic exposure. No hybridization was detected to *Drosophila* DNA.

The 2.1 kb ApaI fragment of CDMP-1 was used as a hybridization probe on Southern blots to type mouse genomic DNAs from two genetic crosses: (NFS/N or C58/J x *M. m. musculus*) x *M. m. musculus* (see Joseph et al., *Mol. Immunol.* 30:733 (1990)) and (NFS/N x *M. spretus*) x *M. spretus* or C58/J (see Adamson et al., *Virology* 183:778 (1991)). DNAs from these crosses have
30 been typed for over 650 markers including the Chr 2 markers *Snap* (synaptosomal associated protein 25), *Psp* (parotid secretory protein), *Emv15* (ecotropic murine leukemia virus 15), *Src* (src oncogene), and *Cd40* (cluster designation 40). Probes for these markers and restriction fragment length polymorphisms used to type these crosses have been described by Joseph et al., in *Mol. Immunol.* 30:733 (1990) and by Grimaldi et al., in *J. Immunol.* 149:3921 (1992). *Src* was typed
35 using a mouse *Src* probe obtained from E. Rassart (U. Quebec, Montreal) following XbaI digestion in the *musculus* cross and BamHI digestion in the *spretus* cross.

Results from Southern blotting with the 2.1 kb cDNA described above identified EcoRI fragments of 7.1 and 2.0 kb in *M. spretus* and *M. m. musculus* and 6.8 and 3.2 kb in NFS/N and C58/J.

Inheritance of the polymorphic fragments in the progeny of the two crosses used for mapping was compared with inheritance of over 650 markers previously mapped to all 19 autosomes and the X chromosome. The gene encoding CDMP-1 was found to be linked to markers on Chr 2 just proximal to Src. The closest linkage was observed with *Psp* and *Emv15*. No recombination was observed between *Cdmp1* and *Psp* in the 100 mice typed for both markers indicating that these genes are within 3.0 cM at the 95% confidence level. Similarly, the absence of recombination between *Gdf5* (Storm et al., *Nature* 368:639 (1994)) and *Cdmp1* in 125 mice suggested these genes colocalized within 2.4 cM. This map location suggested close proximity to the brachypodism locus (*bp*). A genetic map that presents the localization of CDMP-1 on chromosome 2 is shown in Figure 3. Recombination fractions are given to the right of each map of the diagram for each adjacent locus pair or cluster. Numbers in parenthesis represent the percent recombination and standard error calculated as described by Green in Genetics and Probability in Animal Breeding Experiments, Oxford University Press, New York (1981). The map on the left is an abbreviated version of the Chr 2 Committee Map disclosed by Siracusa et al., in *Mammal Genome* 4:S31 (1993), and shows the map location of *bp* relative to the other markers typed in the crosses used here.

The brachypodism (*bp* mice) disorder is characterized by a distinct shortening of the limbs without other tissue abnormalities. The defect has previously been attributed to lack of production of a chondrogenic signal by mesenchymal cells at the time of chondrogenesis (Owens et al., *Dev. Biol.* 91:376 (1982)). During the course of our investigation, an independent study by Storm et al. (*Nature* 368:639 (1994)) described the isolation of the mouse CDMP-1 homolog, called *Gdf-5*, and established its linkage to the brachypodism (*bp*) mutation. The types of mutations observed in *bp* mice were found to be effective null-mutations for the gene encoding *Gdf-5*/CDMP-1. The pattern of expression of CDMP-1 throughout the cartilaginous core observed during human embryonic long bone development, coupled with the *bp* mutation in mice, indicated that its primary physiological role was most likely at the stage of early chondrogenesis and chondrocyte differentiation in the developing limb.

The foregoing results indicated the CDMP-1 and CDMP-2 cDNAs were novel, exhibited moderate sequence conservation across species as judged by evolutionary hybridization studies and that the CDMP-1 gene localized to mouse chromosome 2. We proceeded to examine the pattern of CDMP expression at the mRNA level.

Example 6 demonstrates the methods used to determine the pattern of CDMP mRNA expression.

Example 6

CDMPs are Predominantly Expressed in Cartilage

During Postnatal Life

Equal amounts of poly(A)⁺ RNA (2 µg) from bovine cricoid and articular cartilage were
5 electrophoresed on 1.2% agarose-formaldehyde gels and then transferred to Nytran membranes
(Schleicher and Schuell, Kenne, NH) according to standard laboratory procedures. Multiple Tissue
Northern blots were obtained from Clontech (Palo Alto, CA). The membranes were prehybridized
for 3 hours at 42°C in hybridization buffer (5 x SSPE, 5 x Denhardt's solution, 50% formamide,
1% SDS and 100 µg/ml freshly denatured salmon sperm DNA). Hybridizations with [³²P]dCTP
10 labeled probes, having specific activities of at least 1 x 10⁹ CPM/µg, were performed overnight
under the same conditions as the prehybridization. Probes included the cDNA probe for human
glyceraldehyde-3-phosphate dehydrogenase (1.1 kb, G3PDH (Clontech, Palo Alto, CA), an Apal
fragment (bp 470 - 1155) of CDMP-1, and an Apal fragment (bp 194 - 677) of CDMP-2. The
CDMP-1 and CDMP-2 probes were chosen to avoid the highly conserved carboxy-terminal
15 domain, thereby minimizing the potential for cross hybridization with other members of the gene
family. Following hybridization, the filters were washed to a final stringency of 55°C, 0.4 x SSC,
0.1% SDS. The mRNA expression levels were quantified using a Phosphorimager (Molecular
Dynamics, Sunnyvale, CA).

Results from Northern analyses of a number of postnatal tissues indicated that CDMP-1
20 could predominantly be detected in newborn articular and cricoid cartilage. In both cases a single
mRNA transcript of approximately 3 kb was observed. The CDMP-1 mRNA was not detected in
pancreas, kidney, skeletal muscle, liver, lung, placenta, brain or heart. In contrast, BMP-3 and
BMP-7 transcripts were detected in subsequent hybridizations of the same blots in mRNA samples
from lung, kidney, brain and small intestine. This finding was consistent with previous results
25 disclosed by Vukicevic et al., (*J. Histochem. Cytochem.* 42:869 (1994)). CDMP-2 mRNA was
detected in postnatal bovine articular and cricoid cartilage as a 4.6 kb mRNA band. After
prolonged exposure, weak hybridization signals were detected at 4.6 kb and 4.0 kb in mRNA from
colon and small intestine, skeletal muscle and placenta.

Two other procedures were used to localize and visualize expression of the CDMP-1 and
30 CDMP-2 gene products. These approaches relied on detection of mRNA and protein in tissue
sections prepared for analysis by microscopy.

Example 7 describes the methods used to demonstrate the preferential expression of
CDMPs during human embryogenesis.

Example 7

CDMPs are Preferentially Expressed in the Cartilaginous Cores of Long Bone During Human Embryogenesis

5 In Situ Hybridization

Tissues from human embryos were obtained after pregnancy termination at from 5 to 14 weeks of gestation. Embryo age was estimated in weeks (W) on the basis of crown-rump length (CRL) and pregnancy records of the conceptual age. They were fixed in 4% paraformaldehyde in 0.1 M phosphate buffer (pH 7.2), embedded in paraffin, sectioned serially at 5-7 μ m, and
10 mounted on silanated slides. The tissues used in the present study were obtained from legally sanctioned procedures performed at the University of Zagreb Medical School. The procedure for obtaining the human autopsy material was approved and controlled by the Internal Review Board of the Ethical Committee at the School of Medicine, University of Zagreb and Office of Human Subjects Research (OHSR) at the National Institutes of Health, Bethesda, MD. *In situ*
15 hybridization was done as described by Vukicevic et al., (*J. Histochem. Cytochem.* 42:869 (1994)) and by Pelton et al. (*Development* 106:759 (1989)). Briefly, sections were incubated overnight at 50°C in a humidified chamber in 50% formamide, 10% dextran sulfate, 4 x SSC, 10 mM dithiothreitol, 1 x Denhardt's solution, 500 μ g/ml of freshly denatured salmon sperm DNA and yeast tRNA with 0.2-0.4 ng/ml 35 S labeled riboprobe (1 x 10⁹ CPM/ μ g). Apal fragments of
20 CDMP-1 and of CDMP-2 (described above) from the pro region, subcloned in both sense and anti-sense direction into pBluescript II (SK)⁺ vector (Stratagene, CA), were used as transcription templates. Riboprobes were then prepared using T7 RNA polymerase (Sure Site Kit, Novagen, Madison, WI) according to the manufacturer's instructions and used with and without prior alkaline hydrolysis. After hybridization, the sections were washed as described by Lyons et al., in
25 *Development* 109:833 (1990), to a final stringency of 0.1 x SSC, 65°C for 2 x 15 minutes. After dehydration through a graded ethanol series containing 0.3 M ammonium acetate, slides were covered with NTB-2 emulsion (Kodak) and exposed between 1 and 3 weeks. After development, the slides were stained with 0.1% toluidine blue, dehydrated, cleared with xylene and mounted with Permount.

30 Immunostaining

A polyclonal antibody to the peptide QGKRPSKNLKARC (SEQ ID NO:10) (amino acids 388-400; prepared by Peptide Technologies, Gaithersburg, MD), which belongs to the mature secreted protein of CDMP-1, was raised in rabbits. Before immunization, the peptide was conjugated to Imject^R Maleimide Activated Keyhole Limpet Hemocyanin (Pierce, Rockfor, IL).
35 Searches performed using the BLAST (Altschul et al., *J. Mol. Biol.* 215:403 (1990)) network service available through the National Center for Biotechnology Information indicated that the

peptide does not show sequence identity with any known protein or BMP. The embryonic tissue sections were stained as recommended by the manufacturer using immunogold as a detection system (Auroprobe LM; Janssen, Belgium) and counterstained with 0.1% toluidine blue. The primary antibody (crude antiserum) was used at a concentration of 15 µg/ml in PBS with 0.5% bovine serum albumin (BSA) for 1 hour. In the controls, the primary antibody was replaced with BSA, normal rabbit serum, or secondary antibody alone.

Results indicated that, at 6 weeks of gestation, CDMP-1 transcripts were detected in precartilaginous condensations within the developing limbs. At 7.5 - 8.5 weeks of gestation, CDMP-1 mRNA expression was found in the cartilaginous cores of long bones, including the articular surfaces. In areas of active cartilage degradation and bone matrix formation, CDMP-1 expression was also detected in hypertrophic chondrocytes. Remarkably, no expression was detected in the axial skeleton and only low mRNA levels were observed in other tissues, such as distal convoluted tubules of the developing kidney, brain and placenta. Immunohistochemical staining indicated that CDMP-1 protein colocalized with the mRNA. However, in addition to the sites of transcription, the protein was also found in the surrounding cartilaginous matrix and in osteoblast-like cells from the primary ossification centers of long bones.

Between 9 and 10 weeks of gestation, CDMP-2 expression was predominantly localized in the more mature and hypertrophic chondrocytes in regions of invasion by blood vessels through the periosteal bony collar of the developing long bone. Again, as for CDMP-1, no hybridization was detected in the vertebral bodies in the corresponding sections and stages of human embryonic development. Low expression levels were detected in the periosteum.

The expression pattern of CDMP-2 suggests it is involved in the terminal differentiation of chondrocytes (hypertrophic and mineralizing) and at the earliest stages of endochondral bone formation, including angiogenesis and osteoblast differentiation. In addition, the relatively high levels of expression (detectable in total RNA blots) in postnatal cartilage suggest possible roles in the maintenance and stabilization of the cartilage phenotype after birth.

We have also designed experiments aimed at determining whether all of the chondrogenic activity contained in cartilage extracts can be attributed to the proteins encoded by the CDMP-1 and CDMP-2 cDNAs. Our approach involves the production and use of neutralizing antibodies using synthetic peptides or recombinant CDMP-1 and CDMP-2 proteins as immunogens. Antibodies raised against these peptides or proteins will be tested for their ability to deplete cartilage extracts of chondrogenic activity. If antibodies specific for the recombinant proteins fail to deplete the extracts of cartilage-forming activity, then residual activity will be due to factors within the extract that are separate from proteins encoded by the CDMP-1 and CDMP-2 proteins. Alternatively, if antibodies raised against the peptides or recombinant proteins can remove

cartilage-inducing activity from the extracts, this will confirm that CDMP-1 and/or CDMP-2 must be responsible for the active agents contained in the extracts.

Example 8 describes the methods that will be used to raise antibodies against synthetic peptides and recombinant CDMP-1 and CDMP-2 proteins. Antibodies produced in this fashion
5 will be tested for their ability to deplete extracts containing CDMP activity.

Example 8

Production and Use of Anti-CDMP Antibodies

Specific monoclonal and polyclonal antibodies will be raised against peptides designed from the mature protein of the CDMPs. Preferentially, the region between the protein cleavage
10 site and the first cysteine of the CDMP-1 and CDMP-2 proteins will be used to design the peptides. In addition, the cDNAs encoding the mature region of the CDMPs will be subcloned in the bacterial pET expression vector, and expressed as monomers in the bacterial expression system. The protein expressed in this system will be used to raise additional antibodies, and to determine the immunoreactivity of the various antisera in Western blots. The bacterially expressed
15 monomers will be refolded into biologically active dimers using standard protocols. This approach may afford another source of recombinant protein.

The antisera obtained in this fashion will be used to further establish the synthesis of the CDMPs by chondrocytes *in vivo* and *in vitro*, and to link the cloned CDMPs to the chondrogenic activity found in cartilage extracts. Conditioned media obtained from chondrocyte cultures and
20 partially purified chondrogenic cartilage extracts after heparin sepharose affinity chromatography, molecular sieve chromatography and Con A chromatography, will be analyzed for the presence of CDMPs by Western blot analysis. Due to the possible heterogeneity of the highly purified chondrogenic cartilage extracts, the antibodies will be used to reduce or deplete the chondrogenic/osteogenic activity in purified fractions in a standard immunoprecipitation
25 experiment.

An important aspect of our invention regards the production and use of recombinant proteins that possess the biological activities of the CDMPs. The following Example describes methods and results that illustrate the production of recombinant CDMP-1 and CDMP-2 in transfected 293 cells, COS-1 cells, and CHO-1 cells. We discovered that 293 cells express BMP-7
30 that could conceivably contaminate preparations of recombinant CDMPs. To avoid possible ambiguities in the interpretation of our results, recombinant CDMP-1 produced in COS-1 cells was used to demonstrate cartilage forming activity. Although the production of recombinant CDMPs in this fashion was rather inefficient, the key finding illustrated by our results was that recombinant protein had the desired cartilage-forming activity. Unexpectedly, and in contrast to the related
35 BMPs, recombinant CDMP-1 induced cartilage formation without noticeable bone formation.

Example 9 describes the procedures used to produce recombinant CDMP proteins. The results presented in the Example confirm that the recombinant cartilage-derived proteins stimulated cartilage formation.

Example 9

Production of Recombinant CDMPs and Assessment of Bioactivity

Full length CDMP-1 was subcloned into the mammalian expression vector pcDNA3 (Invitrogen Corporation, San Diego, CA) containing the cytomegalovirus early gene promotor and other elements required for expression in mammalian cells. COS 1 cells were cultured in Opti-MEM I (Gibco/BRL, Gaithersburg, MD) in the presence of 5% fetal bovine serum and antibiotics. The cells were grown to approximately 70-80% confluency in 150 mm dishes and transfections of the respective plasmids (20 µg plamid) were carried out by the calcium phosphate method using the transfection MBS mammalian transfection kit (Stratagene, La Jolla, CA). The cells were incubated with the calcium phosphate-DNA mixture for 3 hours at 35°C. Supernatants were removed and the plates were washed 3 times with PBS. 15 ml of Opti-MEM I (serum reduced medium) was added in the absence of serum, and the dishes were incubated overnight. Transfection efficiencies were tested by transfection of a control plasmid, pCMVβ-gal and cell extracts were assayed for β-galactosidase activity. Conditioned media were collected at 24 hour intervals for a period of 96 hours. The pooled media was centrifuged to remove cell debris and then concentrated using Mascrosep 10 concentrators (Filtron Technology Inc., Northborough, MA). Further purification of recombinantly expressed protein was performed as described in preceding Examples. In one exemplary procedure, the conditioned media was adjusted to 4 M urea, 25 mM Tris HCl (pH 7.0) and applied to a heparin Sepharose column. The column was washed with the same buffer containing 0.1 M NaCl, and eluted with 1 M NaCl. The heparin Sepharose unbound and eluted fractions were assayed for biological activity as described by Luyten et al., in *J. Biol. Chem.* 264:13377 (1989).

Biological activity of the recombinantly expressed protein was investigated using *in vitro* and *in vivo* chondrogenic/osteogenic assays. For the *in vivo* assay, fractions containing the CDMPs were precipitated with ethanol, or dried onto a carrier such as bone matrix residue (mainly collagen type I particles) and cartilage matrix residue (cartilage tissue after extraction with chaotropic agents, and powderized to particles with a size of 75-400 µm). The dried pellet (about 25 mg) was implanted subcutaneously in rats. Implants were harvested after 11 and 21 days, and analyzed for chondrogenesis/osteogenesis using alkaline phosphatase determinations. Histological analysis of recovered samples was also performed using toluidine blue, alcian blue and safranin O staining.

Results obtained using the recombinant CDMP-1 produced in COS-1 cells revealed chondrogenic activity in this *in vivo* assay. Significantly, no osteogenic activity was observed in

any of the recovered samples. Osteogenic activity would ordinarily have been observed if the same procedures had been carried out using recombinant BMPs. This difference highlighted the unique properties of recombinant CDMP-1.

5 Future *in vitro* chondrogenic experiments will be performed to determine the precursor cells responsive to the CDMPs. Undifferentiated (10T1/2 cells, bone marrow stromal cells, mesenchymal stem cells) and already committed skeletal cells (limb bud cells, perichondrial or periosteal cells, fetal epihyseal chondroblasts, and chondrocytes) will be transfected with the cDNAs or treated with recombinantly expressed CDMPs to evaluate the stage of differentiation associated with the chondrogenic activity of the CDMPs.

10 Future *in vivo* chondrogenic experiments will be directed to expression of large quantities of CDMP-1 and CDMP-2 by stable transfectants. We contemplate the use of hybrid expression constructs in which the pro-region of one BMP family member (for example BMP-2) is operationally linked to the regions encoding the mature CDMPs. We also anticipate *in vivo* assays based on implantation in other sites, apart from subcutaneous implantation, which may reveal
15 distinct or superior biological activities of the CDMPs. For example, we anticipate implantation in the synovial cavity may have utility in such assays.

The CDMPs disclosed in the present invention have important applications in the repair of cartilage defects. We contemplate two general approaches for this type of therapy. In the first place, the CDMPs are used as lineage-specific growth factors for the *ex vivo* expansion of
20 chondrocytes isolated from a donor who requires therapeutic intervention. Following expansion, these cells can be reimplanted into a cartilage lesion in the donor, whereafter repair of cartilage will take place. In a different scenario, CDMPs are introduced into a cartilage lesion. For example, a composition containing an appropriate CDMP or mixture of CDMPs can be implanted into a lesion for the purpose of stimulating *in vivo* chondrogenesis and repair of cartilage. The
25 CDMPs can be combined with any of a number of suitable carriers. An appropriate carrier can be selected from the group comprising fibrin glue, cartilage grafts, and collagens. An implantable mixture can be introduced into the site of a lesion according to methods familiar to those having ordinary skill in the art. In one application, we contemplate that periosteal synovial membrane flap of tissue or inert material can be impregnated with CDMPs and implanted for cartilage repair.

30 Example 10 illustrates one application of the CDMP preparations described above. Specifically, the following Example describes the use of CDMPs to facilitate repair of cartilage in the knee joint.

Example 10Treatment of Deep Knee Defects With Cartilage-
Derived Morphogenetic Proteins

A young patient having a large defect in the articular surface of the knee joint is identified. According to standard surgical procedures, a periosteal flap is obtained from the bone beneath the joint surface of rib cartilage. The tissue flap is pre-soaked in an extract containing CDMPs or alternatively in a solution containing recombinant CDMPs. The periosteal flap treated in this way is then attached over the lesion in the articular surface of the knee joint by a sewing procedure, for example using resolvable material. The joint is then closed. The joint is injected with a solution containing CDMPs dissolved or suspended in a pharmacologically acceptable carrier to maintain the chondrogenic process. Injection is continued until the monitoring physician indicates repair of the cartilage is complete. The patient notices markedly less joint pain as the cartilage repair process progresses. Exam by arthroscopy indicates repair of the lesion within several weeks following the initial procedure.

We also contemplate gene therapy protocols based on expression of CDMP cDNAs or genomic constructs as a way of facilitating *in vivo* cartilage repair. Diseases such as chondromalacia or osteoarthritis are examples for which such gene therapy protocols are contemplated. Therapy may be achieved by genetically altering synoviocytes, periosteal cells or chondrocytes by transfection or infection with recombinant constructs that direct expression of the CDMPs. Such altered cells can then be returned to the joint cavity. We contemplate that gene transfer can be accomplished by retroviral, adenoviral, herpesvirus and adeno associated virus vectors.

Both *in vivo* and *ex vivo* approaches are anticipated for continuously delivering CDMPs for the purpose of retarding ongoing osteoarthritic processes and for promoting cartilage repair and regeneration. In addition, one might employ inducible promoter constructs (e.g. under transcriptional control of a dexamethasone promoter) in gene therapy applications of the present invention. A combined approach to osteoarthritis therapy may have particular advantages. For example, CDMP-2 could be continuously expressed to support the integrity of the articular surface. An inducible construct could be employed to express CDMP-1 so that chondrogenesis could be accelerated at the time of more aggressive destruction.

The foregoing experimental results and characterization confirmed the CDMP-1 and CDMP-2 isolates belong to the TGF- β superfamily. Based on the high percentage identity of their C-terminal domains, CDMP-1 and CDMP-2 can be classified as members of a novel subfamily. Although CDMP-1 and CDMP-2 were identified in two different species (human and bovine), they represent distinct genes since the sequences of their pro-regions are significantly divergent.

Several BMPs have now been implicated in early skeletal development, including BMPs - 2, -4, -5, -7 and CDMP-1 (GDF-5). Other members, such as BMPs -3, -6, -7 and CDMP-2, may be involved in later stages of skeletal formation (13, 15). The role of the BMPs in early development could be chemotactic, mitogenic or inductive. Their function in later stages of skeletal development might be promotion of differentiation and maintenance of the established phenotype. The availability of mouse strains with null mutations in specific BMP members, such as the short-ear mice (*Bmp5*) and the *bp* mice (*Cdmp1/Gdf5*), allows analysis of the specific contributions of the respective members in each of the stages of skeletal development.

The absence of expression of both CDMP-1 and CDMP-2 in the axial skeleton has implications for models of skeletal development. For example, the *bp* mice have disturbed limb development but a normal axial skeleton. This is the first evidence that the developmental mechanisms and differentiation pathways of the vertebral bodies are distinct from those of the peripheral skeletal elements. Further, this indicates the basic form and pattern of the skeleton are likely to be determined by a number of BMP-like signaling molecules.

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WE CLAIM:

1. A purified cartilage extract that stimulates local cartilage formation when combined with a matrix and implanted into a mammal, said extract being produced by a method comprising:
 - (a) obtaining cartilage tissue;
 - 5 (b) homogenizing said cartilage tissue in the presence of chaotropic agents under conditions that permit separation of proteins from proteoglycans;
 - (c) separating said proteins from said proteoglycans; and
 - (d) obtaining said proteins.
- 10 2. The extract of Claim 1, wherein said extract is obtained by a method in which step (c) comprises use of a sepharose column.
3. The extract of Claim 1, wherein said extract is obtained by a method which additionally comprises the steps of separating said proteins on a molecular sieve and obtaining those proteins having a molecular weight between 30 kDa and 60 kDa.
- 15 4. The extract of Claim 1, wherein said extract is an extract of articular cartilage.
5. The extract of Claim 1, wherein said extract is an extract of epiphyseal cartilage.
6. A method of preparing a partially purified articular cartilage extract having chondrogenic activity, comprising the steps:
 - (a) obtaining cartilage tissue;
 - (b) homogenizing said cartilage tissue in the presence of chaotropic agents
 - 20 under conditions that permit separation of proteins from proteoglycans;
 - (c) separating said proteins from said proteoglycans; and
 - (d) obtaining said proteins.
7. The method of Claim 6, wherein step (c) comprises use of a sepharose column.
8. The method of Claim 7, wherein step (c) comprises isolating the proteins that bind
- 25 heparin Sepharose in the presence of 0.15 M NaCl but not in the presence of 1 M NaCl.
9. The method of Claim 6, additionally comprising the steps of separating said proteins on a molecular sieve and obtaining those proteins having a molecular weight between 30 kDa and 60 kDa.
10. An isolated DNA molecule encoding a protein having chondrogenic activity *in vivo* but substantially no osteogenic activity *in vivo*, said molecule having a nucleotide sequence that can hybridize to a polynucleotide having a nucleotide sequence selected from the group consisting of SEQ ID NO:11 and SEQ ID NO:12 at 55°C with 0.4× SSC and 0.1% SDS.
11. The isolated DNA molecule of Claim 10, wherein said molecule has a nucleotide sequence selected from the group consisting of SEQ ID NO:13 and SEQ ID NO:14.

12. A recombinant protein having chondrogenic activity *in vivo* but substantially no osteogenic activity *in vivo*, wherein said protein has an amino acid sequence selected from the group consisting of SEQ ID NO:13 and SEQ ID NO:14.

13. A method of stimulating cartilage formation in a mammal, comprising the steps:

- 5 a) supplying cartilage-derived morphogenetic proteins having *in vivo* chondrogenic activity;
- b) mixing said partially purified proteins with a matrix to produce a product that facilitates administration of said partially purified proteins; and
- c) implanting the product of step (b) into the body of mammal to stimulate
- 10 cartilage formation at the site of implantation.

14. The method of Claim 13, wherein said partially purified cartilage-derived morphogenetic proteins are obtained from articular cartilage or epiphyseal cartilage.

15 15. The method of Claim 13, wherein the matrix of step (b) comprises a cellular material.

 16. The method of Claim 13, wherein mixing step (b) additionally comprises mixing of viable chondroblast or chondrocytes.

 17. The method of Claim 5, wherein the implanting step comprises implanting subcutaneously.

20 18. The method of Claim 5, wherein the implanting step comprises implanting subcutaneously.

 19. The method of Claim 5, wherein the implanting step comprises implanting intramuscularly.

25 20. A composition that can be administered to a mammal for the purpose of stimulating chondrogenic activity at the site of administration without substantially stimulating osteogenic activity, said composition comprising at least one cartilage-derived morphogenetic protein and a matrix.

 21. The composition of Claim 20, wherein said cartilage-derived morphogenetic protein is derived from an extract of cartilage tissue.

30 22. The composition of Claim 20, wherein said cartilage tissue is selected from the group consisting of articular cartilage and epiphyseal cartilage.

 23. The composition of Claim 20, wherein said cartilage-derived morphogenetic protein is a recombinant protein.

 24. The composition of Claim 20, wherein said recombinant protein has a sequence selected from the group consisting of SEQ ID NO:13 and SEQ ID NO:14.

25. The composition of Claim 20, wherein said matrix is selected from the group consisting of fibrin glue, freeze-dried cartilage, collagens and guanidinium-insoluble collagenous residue of demineralized bone.

26. The composition of Claim 20, wherein said matrix is a non-resorbable matrix
5 selected from the group comprising tetracalcium phosphate and hydroxyapatite.

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TCAAGAACGA GTATTTTTCAGT GCTGCTgact GGAGAGGGTG CAGGTCTGGA TACGAGAGCA TTTCACATAT GGGAGTGGAT ACAAACACAC ACCGGCAGCA CTTCAAGAGT TTCAGACTGA
 GGAGAAAC TTTCCCTTCT GCTGCTACTG CTGCTCCGC TGCTTTTGAA AGTCCACTTC CTTTCATGGT TTTCCTGACC AACACAGAG CACCTTCGCT GCTGCCGCTG TTCTCTTTGG
 TTCTATTTCAG CGGCTGGCCA GAGGATGAGA CTCCCAAC TCCTCACTTT CTTGCTTTGG TACCTGGCTT GCGTGGACCT GGAATTCATC TGCACGTGTG TGGGTGCCCC TGACTTGGCC 32
M R L P K L L T F L L W Y L A W L D L E F I C T V L G A P D L G
 CAGAGACCCC AGGGTCCAG GCCAGGATTG GCCAAGCAG AGCCCAAGGA GAGGCCCCCC CTGGCCCGGA ACCTCTTCAG GCCAGGGGT CACAGCTATG GTGGGGGGG CACCAATGCC 72
 Q R P Q G S R P G L A K A E A K E R P P L A R N V F R P G G H S Y G G A T N A
 AATGCAAGG CAAAGGAGG CACGGGGCAG ACAGAGGGCC TGACACAGCC CAAGAGGAT GAAACCAAAA AGTGTCCCCC CAGACCGGGC GGCCTCTAAC CCAAGCCAGG ACACCTCTCC
 N A R A K G G T G Q T G G L T Q P K K D E P K K L P P R P G G P E P K P G H P P 112
 CAAACAGGC AGCTACAGC CCGGACTGTG ACCCCAAAG GACAGCTTCC CGGAGGCAAG GCACCCCAAA AAGCAGATC TGTCTCCAGC TCCTTCTGCT TGAAGAAGGC CAGGAGGCC
 Q T R Q A T A R T V T P K G Q L P G G K A P K A G S V P S S F L L K K A R E P 152
 GGGCCCCAC GAGAGCCAA GGAGCGTTT CCGCCAGCCC CCATCACACC CACAGATAC ATGCTCTGC TGTACAGGAC GCTGTCCGAT GCTGACAGAA AGGAGGCAA CAGCAGCGTG
 G P P R E P K E P F R P P P I T P H E Y M L S L Y R T L S D A D R K G N S S V 192
 AATTCAGG CIGGCTGGC CAACACCATC ACCAGCTTTA TTGACAAAG GCAAGTAC GAGGTCCCG TGCTCAGAA GCAGAGGTAC GTGTTTGACA TTAGTGCCTT GGAGAGGAT
 K L E A G L A N T I T S F I D K G Q D D R G P V V R K Q R Y V F D I S A L E K D 232
 GGGCTGCTGG GGGCCGAGCT GCGATCTTGG CCGAAGAGC CCTCGGACAC GGGTCCCCC GAGGCCCGG GGTGCCCCAG CTGAAGCTGT CCAGCTGCC CAGCGGCCGG
 G L L G A E L R I L R K K P S D T A K P A V P R S R R A A Q L K L S S C P S G R 272
 CAGCCCGCG CTTGCTGGA TGTGCTCC GTGCCAGGC TGGACGATC TGGCTGGAG GTGTTGACA TCTGGAAGCT CTTCGAAAC TTGAAGACT CGGCCAGCT GTGCTGGAG
 Q P A A L L D V R S V P G L D G S G W E V F D I W K L F R N F K N S A Q L C L E 312
 CTGAGGCTT CCGAAGCGG CAGGACCGTG GACCTCCGTG GCTGGGCTT GCACCGGCG GCGGCGAGG TCCACAGAA GGCCTGTTC CTGTTGTTTG GCGGACCAA GAAACGGAC
 L E A W E R G R T V D L R G L G F D R A A R Q V H E K A L F L V F G R T K K R D 352
 CTGTTCTTTA ATGAGATTAA GCGCGCTCT GCGCAGGAG ATAGACGCT GTATGAGTAC CTGTTGAGC AGCGCGGCG CCAATCGCCA CTGCGCAGG CAAGCGACC 392
 L F F N E I K A R S G Q D D K T V Y E Y L F S Q R R K R R A P S A T R Q G K R P
 AGCAAGACC TTAAGGCTCG CTGAGTCCG AAGGCACTCC ATGTCAACTT CAAGCACATG GCTGGGAGC ACTGGATCAT CGACCCCTT GAGTAGAGG CTTTCCACTG CGAGGGGCTG
S K N L K A R C S R K A L H V N F K D M G W D D W I I A P L E Y E A F H C E G L 432
 TCGAGTTCC CATTGGCTC CCACCTGGAG CCACAGATC ATGCACTCAT CCAGACCTTG ATGAACCTGA TGGACCCCGA GTCCACACCA CCCACCTGCT GTGTGCCAC GCGGCTGAGT
C E F P L R S H L E P T N H A V I Q T L M N S M D P E S T P P T C C V P T R L S 472
 CCATACGA TCTCTTCAT TGACTTGGC AACACGTGG TGTATPAGA GTATGAGGAC ATGGTGTGG AGTGTGTGG S C G C R . (SEQ. ID NO.: 11)
 P I S I L F I D S A N N V V Y K Q Y E D M V V E S C G C R . (SEQ. ID NO.: 13) 501
 ACATCCGAG AGCCCTTCC TGCACTCTG GAATCAGA GGGTCAAGA ACCTGGCA GAGCATCTA CACAGCTTGG TGAAGGATT CAAAGCTT CCTGCTCTC TGAGTGTAC
 TTGGGCTAAA GCGCCCTTT TATCCACAAG TTCCCTTGGC TGCGCTTGC CTGATGTGAG CAGTGAGC CAGTGCCA CAGTGTGAG GAGGACAGA CTTGGAATGG GACTGATCC
 CAGAAACAG TGCTTTCCA TGACACTCAG CCCACCATTT CTCTCACT GGGCTTCTC AGCTCTGGA CTCTCTAAG CACCTCTAG GAGGACACA GTGCCACTG CACTCTCAA
 TCACATTGT GCTGTGTAC TTCTGTGCC TGGACAGTT GAGAGCTGA CTGGCAAGA GTGGAGAGA AGAGAGAGG GCTTGTATAG AGTTGAGGAG TGTGAGGCTG TTAGACTGTT
 AGATTAAAT GTATTATGAT GAGTAAAA GCAAACTGT GCCTAAAAA AAAAAAAAAA (SEQ. ID NO.: 11)

FIGURE 1

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CGAGCTCTCG CCGAGCTGG GTCCGCCAAG GGAATCGMA CGCCCAAGGA AGAAGGATG CCAGGAGGCG CCAGAGAGAA TGCCACGGCC CGGAGGCCCC TGATCGCCA GGAGCCCCG 120
 R A S A E L G S A K G M R T R K E G R M P R A P R E N A T A R E P L D R Q E P P
 CCAGGCTGC AGGAGGAGC CCAGGAGCG CCACACAGC AGCTGAGC TCGGAGCCT CCAGGAGGCG CCAGGAGGCG GGTGCCCCAC GAGTACATGC TGTCAATCTA CAGGACTTAC 240
 F R P Q E E P Q R R P F Q Q P E A R E P F G R G P R L V P H E Y M L S I Y R T Y
 TCATCGCG AGAAGCTGG CATCAATGCT AGCTTTTCC AGTCTTCAA GTCGCTANT AGTCACTA GCTTTGTAGA CAGGGAGCTA CACGATCTCT CACACACTCC TCCTCGGAGA 360
 S I A E K L G I N A S F F Q S S K S A N T I T S F V D R G L D D L S H T P L R R
 CAGAATATT TGTGTGATGT GTCCAGGCTC TCAGACAAG AAGAGCTGCT GTCCGCTGCT GTCCGCTGCT GTCCGCTGCT GTCCGCTGCT GTCCGCTGCT GTCCGCTGCT 480
 Q K Y L F D V S T L S D K E E L V G A D V R L F R Q A P A A L A P P A A A P L A
 GTCTCTGCC TCACGTCGC CCTCTGCT GAGGCGCG AGCTTGACC CCGAGGCGG CCGGCGCGG CCGGCGCGG CCGGCGCGG CCGGCGCGG CCGGCGCGG 600
 A L R L P V A P A A G S A E P G P A G A P R P G W E V F D V W R G L R P Q P W K
 CACCTCTGCT TGGAGCTTC GCGCGCTGG GCGCGCGAGC CCGCGCGCG CCGCGCGCG CCGCGCGCG CCGCGCGCG CCGCGCGCG CCGCGCGCG CCGCGCGCG 720
 Q L C L E L R A A W G G E P G A A E D E A R T P G P Q Q P P P P D L R S L G F G
 CGAGGCTGC GACCCGCCA GAGGCGCGC TTCTCTGCTG TGTCTCCAG GTCCAGCGC AAGACCTGT TCGCGGAGAT GCGCGAGCAG CTGGGCTCG CGACCGAGT GGTGCGGCC 840
 R R V R T P Q E R A L L V V F S R S Q R K T L F A E M R E Q L G S A T E V V G P
 GTGTGTTGG CCGAGGCTC GCGCGCGCG CCGCGCGCG CCGCGCGCG CCGCGCGCG CCGCGCGCG CCGCGCGCG CCGCGCGCG CCGCGCGCG CCGCGCGCG 960
 G G A E G S G P P P P P P P P P P P S P S P G R R R T A F A
 AGCTCCAGC GCAAGCGCA CCGCAAGAG TCGAGCTGC GCTCGACAA GAAGCCCTG CAGCTGAAT TCAAGGAGT GCGTGGGAC GACTGGATTA TCGCCCGCT GGAGTAGGAG 1080
 S R H G K R H G K K S R L R C S K K P L H V N F K E L G W D D W L I A P L E Y E
 GCTACCACT CCGAGGCGT GTGCGCTTC CCGTACGCT CCGACTGGA GCGGACCAAC CAGCCATCA TCCAGACCT GATGACTCC ATGACCCCG GGTCCACGCC GCGAGCTGC 1200
 A L H C E S V S D E P L R S H L E P T N H A J L Q T L M N S M D P G S T P P S C
 TCGTGGCCA CCAATTGAC TCCATCAGC ATCTGTACA TCGAGCGCG CCAATATGT GTCTACAAG AGTACAGGA GATGTGTGTG GATGCTGCG GCTGCGAG 1308
 V F T K L T P I S I L Y I D A G N N V V Y N E Y E E M V V E S C G C R

FIGURE 2

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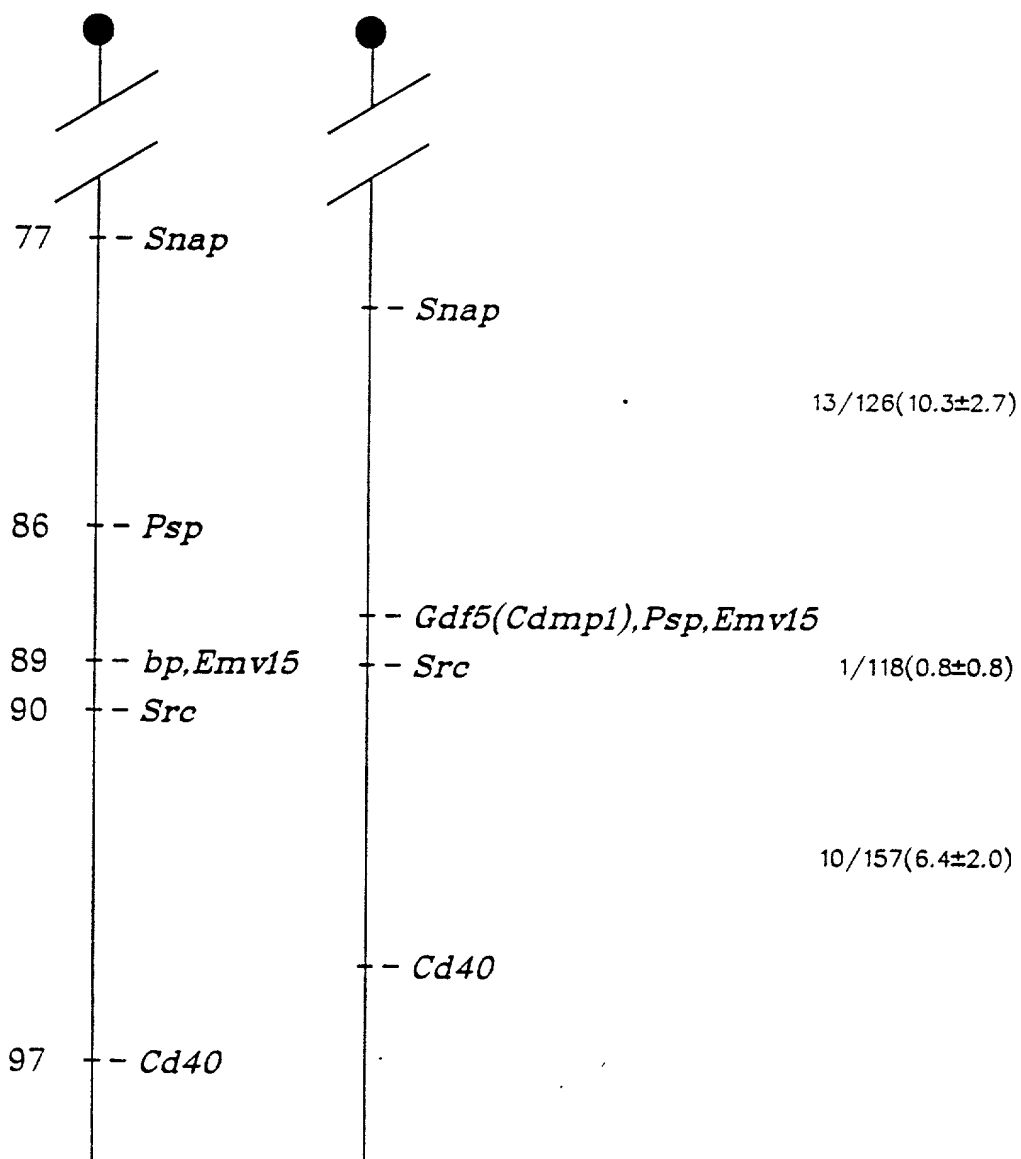


FIG. 3

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Xenopus CDMF-x	WI	I	APL	E	YEA	H	HCEG	V	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:16)
Human CDMF-1	WI	I	APL	E	YEA	F	HCEG	D	C	E	FP	LRSHLEPTNH	A	(SEQ ID NO:17)
Chicken CDMF-x	WI	I	APL	E	YEA	Y	HCEG	D	C	E	FP	LRSHLEPTNH	A	(SEQ ID NO:18)
Zebrafish CDMF-3	WI	V	APL	D	YEA	Y	HCEG	V	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:19)
Xenopus CDMF-x	WI	I	APL	E	YEA	Y	HCEG	V	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:20)
Human CDMF-2	WI	I	APL	E	YEA	Y	HCEG	V	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:21)
Bovine CDMF-2	WI	I	APL	E	YEA	Y	HCEG	V	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:22)
Zebrafish CDMF-x	WI	M	APL	D	YEA	Y	HCEG	D	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:23)
Consensus	WI	I	APL	E	YEA	Y	HCEG	V	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:24)

FIGURE 4

DECLARATION AND POWER OF ATTORNEY - USA PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name;

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled "**CARTILAGE-DERIVED MORPHOGENETIC PROTEINS**"; the specification of which was filed on **May 1, 1997** as Application Serial No. **08/836,081**.

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above;

I acknowledge the duty to disclose to the U.S. Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, § 1.56;

I hereby claim foreign priority benefits under Title 35, United States Code, § 119 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

PRIOR FOREIGN APPLICATION(S)

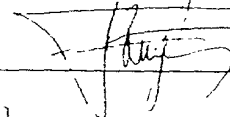
Priority
Claimed

No.: **PCT/US94/12814** Country: **PCT** Date Filed: **11/07/94** Yes

POWER OF ATTORNEY: I hereby appoint the following attorneys and/or agents to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith (if this application is assigned, I acknowledge that the appointed individuals do not represent me, and that instead they represent the assignee): James C. Haight, 25,588; Gloria H. Richmond, 30,416; David R. Sadowski, 32,808; Robert Benson, 33,612; Jack Spiegel, 34,477; Laurence J. Hyman, 35,551; Susan S. Rucker, 35,762; Stephen L. Finley, 36,357; Larry M. Tiffany, 40,844; Steven Ferguson, 38,448; and John Peter Kim, 38,514, as principal attorneys.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful, false statements may jeopardize the validity of the application or any patent issued thereon.

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Inventor's signature 

Date 6/25/87

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Full name of second inventor: **MALCOLM MOOS, JR.**

Inventor's signature Malcolm Moos Jr. M.D., Ph.D.

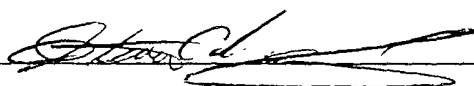
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Inventor's signature 

Date 7/1/97

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Citizenship: ~~Taiwan~~ United States of America 

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NSB-4555 lmd 061997

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Moos, Jr., Malcolm
Chang, Steven Chao-Huan
- (ii) TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
PROTEINS
- (iii) NUMBER OF SEQUENCES: 24
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(B) STREET: 620 Newport Center Drive, 16th Floor
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(F) ZIP: 92660
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows
(D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/836,081
(B) FILING DATE: 28-JUL-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Bartfeld, Neil S
(B) REGISTRATION NUMBER: 39,901
(C) REFERENCE/DOCKET NUMBER: NIH099.001APC
- (ix) TELECOMMUNICATION INFORMATION:
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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
 (ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 3...21
- (D) OTHER INFORMATION: inosine

- (A) NAME/KEY: Other
- (B) LOCATION: 24...24
- (D) OTHER INFORMATION: A or C or G or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGNFGGMANG AYTGGATHRT NGCNCC

26

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 3...3
- (D) OTHER INFORMATION: Xaa = Q or N

- (A) NAME/KEY: Other
- (B) LOCATION: 7...7
- (D) OTHER INFORMATION: Xaa = I or V

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly Trp Xaa Asp Trp Ile Xaa Ala Pro
 1 5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 3...24
- (D) OTHER INFORMATION: inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGNTGGWSNG ARTGGATHAT NWGNCC

26

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gly Trp Ser Glu Trp Ile Ile Ser Pro
1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 9...9
- (D) OTHER INFORMATION: A or T or G or C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AARRGTYTGNA CRATRGCRTG RTT

23

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asn His Ala Ile Val Gln Thr Leu

1

5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 3...18
- (D) OTHER INFORMATION: inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CANSCRCANS HNYBNACNAY CAT

23

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 2...2
- (D) OTHER INFORMATION: Xaa = V or I

- (A) NAME/KEY: Other
- (B) LOCATION: 4...4
- (D) OTHER INFORMATION: Xaa = E or R

D00150-6742360

- (A) NAME/KEY: Other
- (B) LOCATION: 5...5
- (D) OTHER INFORMATION: Xaa = G or S or A

- (A) NAME/KEY: Other
- (B) LOCATION: 7...7
- (D) OTHER INFORMATION: Xaa = G or A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Xaa Val Xaa Xaa Cys Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 2...2
- (D) OTHER INFORMATION: Xaa = any aa

- (A) NAME/KEY: Other
- (B) LOCATION: 3...3
- (D) OTHER INFORMATION: Xaa = any aa

- (A) NAME/KEY: Other
- (B) LOCATION: 4...4
- (D) OTHER INFORMATION: Xaa = R or A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Arg Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

006750" 67842560

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala Arg Cys
 1 5 10

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCAAGAACGA	GTTATTTTCA	GCTGCTGACT	GGAGACGGTG	CACGTCTGGA	TACGAGAGCA	60
TTTCCACTAT	GGGACTGGAT	ACAAACACAC	ACCCGGCAGA	CTTCAAGAGT	TTCAGACTGA	120
GGAGAAAACC	TTTCCCTTCT	GCTGCTACTG	CTGCTGCCGC	TGCTTTTGAA	AGTCCACTTC	180
CTTTCATGGT	TTTTCCTGCC	AAACCAGAGG	CACCTTCGCT	GCTGCCGCTG	TTCTCTTTGG	240
TGTCATTGAG	CGGCTGGCCA	GAGGATGAGA	CTCCCCAAAC	TCCTCACTTT	CTTGCTTTGG	300
TACCTGGCTT	GGCTGGACCT	GGAATTCATC	TGCACTGTGT	TGGGTGCCCC	TGACTTGGGC	360
CAGAGACCCC	AGGGGTCCAG	GCCAGGATTG	GCCAAAGCAG	AGGCCAAGGA	GAGGCCCCCC	420
CTGGCCCCGA	ACGTCTTCAG	GCCAGGGGGT	CACAGCTATG	GTGGGGGGGC	CACCAATGCC	480
AATGCCAGGG	CAAAGGGAGG	CACCGGGCAG	ACAGGAGGCC	TGACACAGCC	CAAGAAGGAT	540
GAAACCAAAA	AGCTGCCCCC	CAGACCGGGC	GGCCCTGAAC	CCAAGCCAGG	ACACCCTCCC	600
CAAAACAAGG	AGGCTACAGC	CCGGAAGTGT	ACCCCAAAAG	GACAGCTTCC	CGGAGGCAAG	660
GCACCCCCAA	AAGCAGGATC	TGTCCCCAGC	TCCTTCCTGC	TGAAGAAGGC	CAGGGAGCCC	720
GGGCCCCCAC	GAGAGCCCAA	GGAGCCGTTT	CGCCACCCC	CCATCACACC	CCACGAGTAC	780
ATGCTCTCGC	TGTACAGGAC	GCTGTCCGAT	GCTGACAGAA	AGGGAGGCAA	CAGCAGCGTG	840
AAGTTGGAGG	CTGGCCTGGC	CAACACCATC	ACCAGCTTTA	TTGACAAAGG	GCAAGATGAC	900
CGAGGTCCCG	TGGTCAGGAA	GCAGAGGTAC	GTGTTTGACA	TTAGTGCCCT	GGAGAAGGAT	960
GGGCTGCTGG	GGGCCGAGCT	GCGGATCTTG	CGGAAGAAGC	CCTCGGACAC	GGCCAAGCCA	1020
GCGGTCCCCC	GGAGCCGGCG	GGCTGCCCAG	CTGAAGCTGT	CCAGCTGCCC	CAGCGGCCCG	1080
CAGCCGGCCG	CCTTGCTGGA	TGTGCGCTCC	GTGCCAGGCC	TGGACGGATC	TGGCTGGGAG	1140
GTGTTTCGAC	TCTGGAAGCT	CTTCCGAAAC	TTTAAGAACT	CGGCCAGACT	GTGCCTGGAG	1200
CTGGAGGCCT	GGGAACGGGG	CAGGACCGTG	GACCTCCGTG	GCCTGGGCTT	CGACCGCGCC	1260
GCCCGGCAGG	TCCACGAGAA	GGCCCTGTTC	CTGGTGTTTG	GCCGCACCAA	GAAACGGGAC	1320
CTGTTCTTTA	ATGAGATTAA	GGCCCGCTCT	GGCCAGGACG	ATAAGACCGT	GTATGAGTAC	1380
CTGTTTCAGC	AGCGGCGAAA	ACGGCGGGCC	CCATCGGCCA	CTCGCCAGGG	CAAGCGACCC	1440
AGCAAGAACC	TTAAGGCTCG	CTGCAGTCGG	AAGGCACTGC	ATGTCAACTT	CAAGGACATG	1500
GGCTGGGACG	ACTGGATCAT	CGCACCCCTT	GAGTACGAGG	CTTTCCACTG	CGAGGGGCTG	1560
TGCGAGTTCC	CATTGCGCTC	CCACCTGGAG	CCCACGAATC	ATGCAGTCAT	CCAGACCCCTG	1620
ATGAACTCGA	TGGACCCCGA	GTCCACACCA	CCCACCTGCT	GTGTGCCCAC	GCGGCTGAGT	1680
CCCATCAGCA	TCCTCTTCAT	TGACTCTGCC	AACAACGTGG	TGTATAAGCA	GTATGAGGAC	1740
ATGGTCGTGG	AGTCGTGTGG	CTGCAGGTAG	CAGCACTGGC	CCTCTGTCTT	CCTGGGTGGC	1800
ACATCCCAAG	AGCCCCCTTC	TGCACTCCTG	GAATCACAGA	GGGGTCAGGA	AGCTGTGGCA	1860
GGAGCATCTA	CACAGCTTGG	TGAAGGGATT	CAATAAGCTT	GCTCGCTCTC	TGAGTGTGAC	1920
TTGGGGCTAAA	GGCCCCCTTT	TATCCACAAG	TTCCCCTGGC	TGAGGATTGC	TGCCCCGTCTG	1980

CTGATGTGAC	CAGTGGCAGG	CACAGGTCCA	GGGAGACAGA	CTCTGAATGG	GACTGAGTCC	2040
CAGGAAACAG	TGCTTTCCGA	TGAGACTCAG	CCCACCATT	CTCCTCACCT	GGGCCTTCTC	2100
AGCCTCTGGA	CTCTCCTAAG	CACCTCTCAG	GAGAGCCACA	GGTGCCACTG	CCTCCTCAAA	2160
TCACATTTGT	GCCTGGTGAC	TTCCTGTCCC	TGGGACAGTT	GAGAAGCTGA	CTGGGCAAGA	2220
GTGGGAGAGA	AGAGGAGAGG	GCTTGGATAG	AGTTGAGGAG	TGTGAGGCTG	TTAGACTGTT	2280
AGATTTAAAT	GTATATTGAT	GAGATAAAAA	GCAAACTGT	GCCTAAAAAA	AAAAAAAAAA	2340
A						2341

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAGGCTCCG	CCGAGCTGGG	CTCCGCCAAG	GGAATGCGAA	CGCGCAAGGA	AGGAAGGATG	60
CCGGGGGCGC	CGAGAGAGAA	TGCCACGGCC	CGGGAGCCCC	TGGATCGCCA	GGAGCCCCCG	120
CCGAGGCCGC	AGGAGGAGCC	CCAGCGGCGG	CCGCCACAGC	AGCCTGAAGC	TCGGGAGCCT	180
CCCCGCAGGG	GCCCGCGCTT	GGTGCCCCAC	GAGTACATGC	TGTCAATCTA	CAGGACTTAC	240
TCCATCGCCG	AGAAGCTGGG	CATCAATGCT	AGCTTTTTC	AGTCTTCCAA	GTCCGGCTAAT	300
ACGATCACTA	GCTTTGTAGA	CAGGGGACTA	GACGATCTCT	CGCACACTCC	TCTCCGGAGA	360
CAGAAGTATT	TGTTTGTATG	GTCCACGCTC	TCAGACAAAG	AAGAGCTGGT	GGGCGCGGAC	420
GTGCGGCTGT	TTCGCCAGGC	GCCCGCTGCC	CTGGCGCCGC	CGGCGGCCGC	TCCGCTTGCA	480
GCTCTTCGCC	TGCCAGTCGC	CCCTGCTGCT	GGAAGCGCGG	AGCCTGGACC	CGCAGGGGCG	540
CCCCGGCCCC	GCTGGGAAGT	CTTCGACGTG	TGGCGGGGCC	TGCGCCCCCA	GCCCTGGAAG	600
CAGCTGTGCT	TGGAGCTTCG	GGCCGCGTGG	GGCGGCGAGC	CGGGCGCCGC	GGAGGACGAG	660
GCGCGCACGC	CTGGGCCCCA	GCAGCCGCCG	CCCCCGGACC	TGCGGAGTCT	GGGCTTCGGC	720
CGGAGGGTGC	GGACCCCCCA	GGAGCGCGCC	TTGCTCGTCG	TGTTCTCCAG	GTCCCAGCGC	780
AAGACCTGT	TCGCCGAGAT	GCGCGAGCAG	CTGGGCTCGG	CGACCGAGGT	GGTCGGCCCC	840
GGTGTGGGG	CCGAGGGGTC	GGGGCCGCCG	CCGCCGCCGC	CGCCGCCGCC	GCCGTCGGGC	900
ACCCCGGACG	CTGGGCTCTG	GTCGCCCTCG	CCTGGCCGGC	GGCGGCGCAC	GGCCTTCGCC	960
AGCCGCCACG	GCAAGCGGCA	CGGCAAGAAG	TCGAGGCTGC	GCTGCAGCAA	GAAGCCCCTG	1020
CACGTGAACT	TCAAGGAGCT	GGGCTGGGAC	GACTGGATTA	TCGCGCCCCT	GGAGTACGAG	1080
GCCTACCACT	GCGAGGGCGT	GTGCGACTTC	CCGCTACGCT	CGCACCTGGA	GCCCACCAAC	1140
CACGCCATCA	TCCAGACGCT	GATGAACTCC	ATGGACCCCG	GCTCCACCCC	GCCCAGCTGC	1200
TGCGTGCCCA	CCAAATTGAC	TCCCATCAGC	ATCTTGTACA	TCGACGCGGG	CAATAATGTG	1260
GTCTACAACG	AGTACGAGGA	GATGGTGGTG	GAGTCGTGCG	GCTGCAGG		1308

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Arg	Leu	Pro	Lys	Leu	Leu	Thr	Phe	Leu	Leu	Trp	Tyr	Leu	Ala	Trp
1				5					10					15	
Leu	Asp	Leu	Glu	Phe	Ile	Cys	Thr	Val	Leu	Gly	Ala	Pro	Asp	Leu	Gly
			20					25					30		
Gln	Arg	Pro	Gln	Gly	Ser	Arg	Pro	Gly	Leu	Ala	Lys	Ala	Glu	Ala	Lys
		35					40					45			
Glu	Arg	Pro	Pro	Leu	Ala	Arg	Asn	Val	Phe	Arg	Pro	Gly	Gly	His	Ser
	50					55					60				
Tyr	Gly	Gly	Gly	Ala	Thr	Asn	Ala	Asn	Ala	Arg	Ala	Lys	Gly	Gly	Thr
65					70					75					80
Gly	Gln	Thr	Gly	Gly	Leu	Thr	Gln	Pro	Lys	Lys	Asp	Glu	Pro	Lys	Lys
				85					90					95	
Leu	Pro	Pro	Arg	Pro	Gly	Gly	Pro	Glu	Pro	Lys	Arg	Gly	His	Pro	Pro
			100					105					110		
Gln	Thr	Arg	Gln	Ala	Thr	Ala	Arg	Thr	Val	Thr	Pro	Lys	Gly	Gln	Leu
		115					120					125			
Pro	Gly	Gly	Lys	Ala	Pro	Pro	Lys	Ala	Gly	Ser	Val	Pro	Ser	Ser	Phe
130						135					140				
Leu	Leu	Lys	Lys	Ala	Arg	Glu	Pro	Gly	Pro	Pro	Arg	Glu	Pro	Lys	Glu
145					150					155					160
Pro	Phe	Arg	Pro	Pro	Pro	Ile	Thr	Pro	His	Glu	Tyr	Met	Leu	Ser	Leu
				165					170					175	
Tyr	Arg	Thr	Leu	Ser	Asp	Ala	Asp	Arg	Lys	Gly	Gly	Asn	Ser	Ser	Val
			180					185					190		
Lys	Leu	Glu	Ala	Gly	Leu	Ala	Asn	Thr	Ile	Thr	Ser	Phe	Ile	Asp	Lys
		195					200					205			
Gly	Gln	Asp	Asp	Arg	Gly	Pro	Val	Val	Arg	Lys	Gln	Arg	Tyr	Val	Phe
210						215					220				
Asp	Ile	Ser	Ala	Leu	Glu	Lys	Asp	Gly	Leu	Leu	Gly	Ala	Glu	Leu	Arg
225					230					235					240
Ile	Leu	Arg	Lys	Lys	Pro	Ser	Asp	Thr	Ala	Lys	Pro	Ala	Val	Pro	Arg
				245					250					255	
Ser	Arg	Arg	Ala	Ala	Gln	Leu	Lys	Leu	Ser	Ser	Cys	Pro	Ser	Gly	Arg
			260					265					270		
Gln	Pro	Ala	Ala	Leu	Leu	Asp	Val	Arg	Ser	Val	Pro	Gly	Leu	Asp	Gly
		275					280					285			
Ser	Gly	Trp	Glu	Val	Phe	Asp	Ile	Trp	Lys	Leu	Phe	Arg	Asn	Phe	Lys
	290					295					300				
Asn	Ser	Ala	Gln	Leu	Cys	Leu	Glu	Leu	Glu	Ala	Trp	Glu	Arg	Gly	Arg
305					310					315					320
Thr	Val	Asp	Leu	Arg	Gly	Leu	Gly	Phe	Asp	Arg	Ala	Ala	Arg	Gln	Val
				325					330					335	
His	Glu	Lys	Ala	Leu	Phe	Leu	Val	Phe	Gly	Arg	Thr	Lys	Lys	Arg	Asp
			340					345					350		
Leu	Phe	Phe	Asn	Glu	Ile	Lys	Ala	Arg	Ser	Gly	Gln	Asp	Asp	Lys	Thr
		355					360					365			
Val	Tyr	Glu	Tyr	Leu	Phe	Ser	Gln	Arg	Arg	Lys	Arg	Arg	Ala	Pro	Ser
	370					375					380				
Ala	Thr	Arg	Gln	Gly	Lys	Arg	Pro	Ser	Lys	Asn	Leu	Lys	Ala	Arg	Cys
385					390					395					400

Ser	Arg	Lys	Ala	Leu	His	Val	Asn	Phe	Lys	Asp	Met	Gly	Trp	Asp	Asp
				405					410					415	
Trp	Ile	Ile	Ala	Pro	Leu	Glu	Tyr	Glu	Ala	Phe	Gly	Cys	Glu	Gly	Leu
			420					425					430		
Cys	Glu	Phe	Pro	Leu	Arg	Ser	His	Leu	Glu	Pro	Thr	Asn	His	Ala	Val
		435					440					445			
Ile	Gln	Thr	Leu	Met	Asn	Ser	Met	Asp	Pro	Glu	Ser	Thr	Pro	Pro	Thr
	450					455					460				
Cys	Cys	Val	Pro	Thr	Arg	Leu	Ser	Pro	Ile	Ser	Ile	Leu	Phe	Ile	Asp
465					470					475					480
Ser	Ala	Asn	Asn	Val	Val	Tyr	Lys	Gln	Tyr	Glu	Asp	Met	Val	Val	Glu
			485						490					495	
Ser	Cys	Gly	Cys	Arg											
			500												

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg	Ala	Ser	Ala	Glu	Leu	Gly	Ser	Ala	Lys	Gly	Met	Arg	Thr	Arg	Lys
1				5					10					15	
Glu	Gly	Arg	Met	Pro	Arg	Ala	Pro	Arg	Glu	Asn	Ala	Thr	Ala	Arg	Glu
			20					25					30		
Pro	Leu	Asp	Arg	Gln	Glu	Pro	Pro	Pro	Arg	Pro	Gln	Glu	Glu	Pro	Gln
		35					40					45			
Arg	Arg	Pro	Pro	Gln	Gln	Pro	Glu	Ala	Arg	Glu	Pro	Pro	Gly	Arg	Gly
50						55					60				
Pro	Arg	Leu	Val	Pro	His	Glu	Tyr	Met	Leu	Ser	Ile	Tyr	Arg	Thr	Tyr
65					70					75					80
Ser	Ile	Ala	Glu	Lys	Leu	Gly	Ile	Asn	Ala	Ser	Phe	Phe	Gln	Ser	Ser
				85					90					95	
Lys	Ser	Ala	Asn	Thr	Ile	Thr	Ser	Phe	Val	Asp	Arg	Gly	Leu	Asp	Asp
			100					105					110		
Leu	Ser	His	Thr	Pro	Leu	Arg	Arg	Gln	Lys	Tyr	Leu	Phe	Asp	Val	Ser
		115					120					125			
Thr	Leu	Ser	Asp	Lys	Glu	Glu	Leu	Val	Gly	Ala	Asp	Val	Arg	Leu	Phe
	130					135					140				
Arg	Gln	Ala	Pro	Ala	Ala	Leu	Ala	Pro	Pro	Ala	Ala	Ala	Pro	Leu	Ala
145					150					155					160
Ala	Leu	Arg	Leu	Pro	Val	Ala	Pro	Ala	Ala	Gly	Ser	Ala	Glu	Pro	Gly
				165					170					175	
Pro	Ala	Gly	Ala	Pro	Arg	Pro	Gly	Trp	Glu	Val	Phe	Asp	Val	Trp	Arg
			180					185					190		
Gly	Leu	Arg	Pro	Gln	Pro	Trp	Lys	Gln	Leu	Cys	Leu	Glu	Leu	Arg	Ala

	195		200		205										
Ala	Trp	Gly	Gly	Glu	Pro	Gly	Ala	Ala	Glu	Asp	Glu	Ala	Arg	Thr	Pro
	210					215					220				
Gly	Pro	Gln	Gln	Pro	Pro	Pro	Pro	Asp	Leu	Arg	Ser	Leu	Gly	Phe	Gly
225					230					235					240
Arg	Arg	Val	Arg	Thr	Pro	Gln	Glu	Arg	Ala	Leu	Leu	Val	Val	Phe	Ser
				245					250					255	
Arg	Ser	Gln	Arg	Lys	Thr	Leu	Phe	Ala	Glu	Met	Arg	Glu	Gln	Leu	Gly
			260					265					270		
Ser	Ala	Thr	Glu	Val	Val	Gly	Pro	Gly	Gly	Gly	Ala	Glu	Gly	Ser	Gly
		275					280					285			
Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Ser	Gly	Thr	Pro	Asp	Ala
	290					295					300				
Gly	Leu	Trp	Ser	Pro	Ser	Pro	Gly	Arg	Arg	Arg	Arg	Thr	Ala	Phe	Ala
305					310					315					320
Ser	Arg	His	Gly	Lys	Arg	His	Gly	Lys	Lys	Ser	Arg	Leu	Arg	Cys	Ser
			325					330						335	
Lys	Lys	Pro	Leu	His	Val	Asn	Phe	Lys	Glu	Leu	Gly	Trp	Asp	Asp	Trp
			340					345					350		
Ile	Ile	Ala	Pro	Leu	Glu	Tyr	Glu	Ala	Tyr	His	Cys	Glu	Gly	Val	Cys
	355						360					365			
Asp	Phe	Pro	Leu	Arg	Ser	His	Leu	Glu	Pro	Thr	Asn	His	Ala	Ile	Ile
	370					375					380				
Gln	Thr	Leu	Met	Asn	Ser	Met	Asp	Pro	Gly	Ser	Thr	Pro	Pro	Ser	Cys
385				390						395					400
Cys	Val	Pro	Thr	Lys	Leu	Thr	Pro	Ile	Ser	Ile	Leu	Tyr	Ile	Asp	Ala
				405				410						415	
Gly	Asn	Asn	Val	Val	Tyr	Asn	Glu	Tyr	Glu	Glu	Met	Val	Val	Glu	Ser
			420				425						430		
Cys	Gly	Cys	Arg												
		435													

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 3...3
- (D) OTHER INFORMATION: Xaa = I or M or V

- (A) NAME/KEY: Other
- (B) LOCATION: 7...7
- (D) OTHER INFORMATION: Xaa = D or E

- (A) NAME/KEY: Other
- (B) LOCATION: 11...11
- (D) OTHER INFORMATION: Xaa = Y or F or H

- (A) NAME/KEY: Other
- (B) LOCATION: 16...16
- (D) OTHER INFORMATION: Xaa = L or V

- (A) NAME/KEY: Other
- (B) LOCATION: 18...18
- (D) OTHER INFORMATION: Xaa = D or E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Trp Ile Xaa Ala Pro Leu Xaa Tyr Glu Ala Xaa His Cys Glu Gly Xaa
 1 5 10 15
 Cys Xaa Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala
 20 25 30

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala His His Cys Ala Gly Val
 1 5 10 15
 Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala
 20 25 30

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu Gly Asp
 1 5 10 15

Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala
 20 25 30

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys Glu Gly Asp
 1 5 10 15
 Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala
 20 25 30

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Trp Ile Val Ala Pro Leu Asp Tyr Glu Ala Tyr His Cys Glu Gly Val
 1 5 10 15
 Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala
 20 25 30

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys Glu Gly Val
 1 5 10 15
 Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala

20

25

30

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Trp	Ile	Ile	Ala	Pro	Leu	Glu	Tyr	Glu	Ala	Tyr	His	Cys	Glu	Gly	Val
1				5					10					15	
Cys	Asp	Phe	Pro	Leu	Arg	Ser	His	Leu	Glu	Pro	Thr	Asn	His	Ala	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Trp	Ile	Ile	Ala	Pro	Leu	Glu	Tyr	Glu	Ala	Tyr	His	Cys	Glu	Gly	Val
1				5					10					15	
Cys	Asp	Phe	Pro	Leu	Arg	Ser	His	Leu	Glu	Pro	Thr	Asn	His	Ala	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Trp	Ile	Met	Ala	Pro	Leu	Asp	Tyr	Glu	Ala	Tyr	His	Cys	Glu	Gly	Asp
1				5					10					15	
Cys	Asp	Phe	Pro	Leu	Arg	Ser	His	Leu	Glu	Pro	Thr	Asn	His	Ala	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Trp	Ile	Ile	Ala	Pro	Leu	Glu	Tyr	Glu	Ala	Tyr	His	Cys	Glu	Gly	Val
1				5				10						15	
Cys	Asp	Phe	Pro	Leu	Arg	Ser	His	Leu	Glu	Pro	Thr	Asn	His	Ala	
			20					25					30		

006T50-6T842560